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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:02:07 ; Search time 43 Seconds
(without alignments)
694.410 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DKQRTINLDQREKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/ECTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2020	99.6	401	US-09-489-847-202	Sequence 202, App
2	2020	99.6	422	US-09-489-847-357	Sequence 357, App
3	631	31.1	148	US-09-673-395A-389	Sequence 389, App
4	168	8.3	3878	US-09-914-259-11	Sequence 11, Appl
5	166.5	8.2	1940	US-09-538-092-901	Sequence 901, App
6	166.5	8.2	1963	US-09-949-016-8888	Sequence 8888, App
7	165.5	8.2	1581	US-09-866-108A-15754	Sequence 15754, A
8	165	8.1	1898	US-08-056-200-94	Sequence 94, Appl
9	165	8.1	1898	US-08-800-644-94	Sequence 94, Appl
10	165	8.1	1898	US-09-538-092-1280	Sequence 1280, Ap
11	161	7.9	1960	US-09-538-092-1077	Sequence 1077, Ap
12	161	7.9	1960	US-09-949-016-10872	Sequence 10872, A
13	160.5	7.9	915	US-09-538-092-863	Sequence 863, App
14	160.5	7.9	916	US-09-949-016-6611	Sequence 6611, Ap
15	160.5	7.9	916	US-09-949-016-11417	Sequence 11417, A
16	160	7.9	1208	US-09-134-000C-5756	Sequence 5756, Ap
17	159.5	7.9	1695	US-09-866-108A-15753	Sequence 15753, A
18	158.5	7.8	1937	US-09-538-092-918	Sequence 918, App
19	158.5	7.8	2107	US-09-949-016-7646	Sequence 7646, Ap
20	158.5	7.8	2107	US-09-949-016-7647	Sequence 7647, Ap
21	157.5	7.8	2101	US-08-466-390-4	Sequence 4, Appl
22	157.5	7.8	2101	US-08-470-950-4	Sequence 4, Appl
23	157.5	7.8	2101	US-08-467-781-4	Sequence 4, Appl
24	157.5	7.8	2101	US-08-195-487-4	Sequence 4, Appl
25	157.5	7.8	2101	US-08-483-924-4	Sequence 4, Appl
26	157.5	7.8	2101	US-09-452-294-1	Sequence 1, Appl
27	157.5	7.8	2101	PCT-US93-06160-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-489-847-202

; Sequence 202, Application US/09489847

; Patent No. 6476195

; GENERAL INFORMATION:

; APPLICANT: Rosen et al

; TITLE OF INVENTION: 98 Human Secreted Proteins

; FILE REFERENCE: P2031P1

; CURRENT APPLICATION NUMBER: US/09/489,847

; CURRENT FILING DATE: 2000-01-24

; EARLIER APPLICATION NUMBER: PCT/US99/17130

; EARLIER FILING DATE: 1999-07-29

; EARLIER APPLICATION NUMBER: 60/094,657

; EARLIER FILING DATE: 1998-07-30

; EARLIER APPLICATION NUMBER: 60/095,486

; EARLIER FILING DATE: 1998-08-05

; EARLIER APPLICATION NUMBER: 60/096,319

; EARLIER FILING DATE: 1998-08-12

; EARLIER APPLICATION NUMBER: 60/095,454

; EARLIER FILING DATE: 1998-08-06

; EARLIER APPLICATION NUMBER: 60/095,455

; EARLIER FILING DATE: 1998-08-06

; NUMBER OF SEQ ID NOS: 376

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 202

; LENGTH: 401

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (307)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-489-847-202

Query Match 99.6%; Score 2020; DB 4; Length 401;

Best Local Similarity 99.5%; Pred. No. 2e-163;

Matches 398; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTYIASSRSVDLQTRIMELEGRVRRRAAERG 60

2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTYIASSRSVDLQTRIMELEGRVRRRAAERG 61

DB

QY 61 AVELKXNEFQGELEKQREQLDKIOSSHNFQLESVKNLYQDEKAVLVNNTTGERLIRVLQ 120

62 AVELKXNEFQGELEKQREQLDKIOSSHNFQLESVKNLYQDEKAVLVNNTTGERLIRVLQ 121

DB

QY 121 DOLKTLQNRGLQODVLQFQKQNTNLERKFSYDLSQCINOMKEVKEOCEERIEBVTKKG 180

122 DOLKTLQNRGLQODVLQFQKQNTNLERKFSYDLSQCINOMKEVKEOCEERIEBVTKKG 181

DB

181	Qy	NEAVASRDLSENNDORQQLALSPQRPQLAAGLPHTPEVQGGKGNVLGNSKSTPAPSSSE	240
182	Db	NEAVASRDLSENNDORQQLALSPQRPQLAAGLPHTPEVQGGKGNVLGNSKSTPAPSSSE	241
241	Qy	VVLDSKRQVKEETNEIIVVNNEEQORLLOEPCREOVVEDRVPVGGRGCGAGELGOTQO	300
242	Db	VVLDSKRQVKEETNEIIVVNNEEQORLLOEPCREOVVEDRVPVGGRGCGAGELGOTQO	301
301	Qy	VQAALSVSQENPEMGPGRDQLVTPDGOEEQEAAAGGRNQOKLGRGDDYNNMDENAEASE	360
302	Db	VQAALSVSQENPEMGPGRDQLVTPDGOEEQEAAAGGRNQOKLGRGDDYNNMDENAEASE	361
361	Qy	TDQAALAGNDRNIDVFNVEDQKQDRTINLLDQREKRNHTL	400
362	Db	TDQAALAGNDRNIDVFNVEDQKQDRTINLLDQREKRNHTL	401

```

RESULT 2
US 09-489-847-357
: Sequence 357, Application US/09489847
: Patent No. 6476195
: GENERAL INFORMATION:
: APPLICANT: Rosen et al
: TITLE OF INVENTION: 98 Human Secreted Proteins
: FILE REFERENCE: P2031P1

```

Query Match	99.6%;	Score 2020;	DB 4;	Length 422;
Best Local Similarity	99.5%;	Pred. No. 2.1e-163;		
Matches 398;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1	MGLNGRRSRKSPPLVLAALVACIIIVGNNWTASSRSVDLQTRIMELEGRRVRAAERG	60		
Db 23	MGLNGRRSRKSPPLVLAALVACIIIVGNNWTASSRSVDLQTRIMELEGRRVRAAERG	82		
Qy 61	AVELKKNEFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNTTGERLIIRVLQ	120		
Db 83	AVELKKNEFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNTTGERLIIRVLQ	142		
Qy 121	DQLKTLQRNTGRLOQDVLFQKQKQTNLERKPSYDLSCINOMKEVKQCEERIIEVTKKG	180		
Db 143	DQLKTLQRNTGRLOQDVLFQKQKQTNLERKPSYDLSCINOMKEVKQCEERIIEVTKKG	202		
Qy 181	NEAVASRDLSENNDORQOLQALSPQRLQAAGLPHTPEVPGCKGNVLGNSKQTPAPSSSE	240		
Db 203	NEAVASRDLSENNDORQOLQALSPQRLQAAGLPHTPEVPGCKGNVLGNSKQTPAPSSSE	262		
Qy 241	VLWDSKRFQVEKEETNEIQVNVNEEQRDLRLOPQPGREQVVEDRPPVGGRGFGGAGELGOTPQ	300		

Db	263	W L D S K R Q V E K E E T N E I Q V N N E E P O R D B L P O E P G R E Q V V D P R P V G G R F G G A G E L G Q I P Q	322
Qy	301	V Q A A L S V S Q E N P E M E G P E R D O L V I P D Q E E E Q E A A G E G R N O O K L R G E D D Y N D M D N E A S E	360
Db	323	V Q A A L X S V S Q E N P E M E G P E R D Q L V I P D Q E E E Q E A A G E G R N O O K L R G E D D Y N D M D N E A S E	382
Qy	361	T D Q A A L A G A N D R N I D V F N V E D Q E K E D T I N L L D Q R E K R N H T L	400
Db	383	T D Q A A L A G A N D R N I D V F N V E D Q E K E D T I N L L D Q R E K R N H T L	422

```

RESULT 3
US-09-673-395A-389
; Sequence 389, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 389
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-389

```

Query Match	31.1%	Score 631	DB 4	Length 148
Best Local Similarity	100.0%	Pred. No. 4.8e-46		
Matches 122	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	279	VEDRPVGGRFGGAGEIGQTPVQAAALSVSENPEMEGPERDQLVIPDQGEESAAAGEG	338	
Db	27	VEDRPVGGRFGGAGEIGQTPVQAAALSVSENPEMEGPERDQLVIPDQGEESAAAGEG	86	
Qy	339	RNQQKLAGEDDYNNDEAESETDKAALAGNDRNIDVFNVEDQKRDITINLLDQREKKNH	398	
Db	87	RNQQKLAGEDDYNNDEAESETDKAALAGNDRNIDVFNVEDQKRDITINLLDQREKKNH	146	
Qy	399	TL 400		
Db	147	TL 148		

```

RESULT 4
US-09-914-259-11
; Sequence 11, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3878
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-11
Query Match      8.3%; Score 168; DB 4; Length 3878;
Best Local Similarity 20.2%; Pred. No. 0.00011;

```

Matches	74;	Conservative	90;	Mismatches	158;	Indels	44;	Gaps	13;
Qy	26	VLGNYNYIASSRSVDLQTRIMELEGRVRRAAAEAGAVELKKNEPQGELEKQREOLD--K 82							
Db	3092	LLEVNIQKQSQMLEMQLVSSMKDRATELQEQLSSEKVVVAELKSELAQTCLKLETTLK 3151							
Qy	83	IQSHNFOLESVN---KLYODEKAVLVNNTTGBERLIRVLOQLKTTQRYNGRIQQ---D 136							
Db	3152	AQHKHLELEAFRLUEVDKTDEVHLLNDTTLASEQKSRLEQWALEKEKAKLGRSEERDK 3211							
Qy	137	VLOFQKQNTNLRKFSYDLSCINOMKEVKEQCEERIEEVTTKGNEAVASRDLSENNDQ 196							
Db	3212	ELEDKFSLESQKQKNILQNLILLEQQKQLINESQOKIE-----SQRMLYDAQQLSEEGCN 3266							
Qy	197	QQLQALSEPOF---RLQAAGLP-----HTEVPQKGNVLGNSKTSQTPAPSEVVLDSSK 248							
Db	3267	LELQVLLSEKVRITREMSSTLDRERLHAQLQSSD---GTGQSRPPLPSEDILLKELQK 3322							
Qy	249	VEKEETNEIQVNVNEEPQDRLPQEPGREGVVEDPVCGRGFGGAGELGQTFQVQAALSV 308							
Db	3323	LEEKHSRIVELLN-ETEKYKLDLSQTRQOMEKQVRHKTL-----QTEQ-EANTEGQ 3373							
Qy	309	QENPEMGPERD---QLVIPDGQEEQEAAGEGRNQOKLRG-EDDYNDMDNEAESETDK 364							
Db	3374	KQWHELOSKVEDLQRL-----BEKQOVVKLDLQGRLOQIMQEFQOKQLEEREKKES 3428							
Qy	365	AALAGN 370							
Db	3429	RILYON 3434							

```

RESULT 5
US-09-538-092-901
; Sequence 901, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 901
; LENGTH: 1940
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P11055
US-09-538-092-901

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	Query Match	8.2%	Score 166.5	DB 4	Length 1940
	Best Local Similarity	23.9%	Pred. No. 5.6e-05		
	Matches	89	Conservative	61	Mismatches 154
					Indels 69
					Gaps 14
Qy	40	DLQTRIMELGRVRRAAAGAVELKNEFQGELEKQREOLDKIQSHNFQLESVKNLYQ	99		
Db	1111	ELGARIEELSEEEAEERATKTKQKSDYARELSEKLEAGGVTSTQIIR-LNKKRE	1169		
Qy	100	DEKAVLVNNTTG-----ERLIRVLQ-----DQLTKLQRYGRLOQDVLVQFNQ	144		
Db	1170	AEFLKLRDLEAATLQHEANVATLRKKHADSVAELEGQIDNLQVRQKLEKSEFKLEI	1229		
Qy	145	TNLERKPSYDLSCINQMKVKGQCEERIEVYTKKNGNEAVASRDLSNNDRQOLQALSE	204		
Db	1230	DDLSSSME-SVSKS KANLEKICRTLEDGEARKNKEE--IQRSLSLTITQKRLQTEAG	1286		

Qy	205	PQPRLOAAGLPHTVEPQGGKGNVLGNSKSTPPAPSSSEVVLDSKROVKEETNETQVNNEEP	264
Db	1287	ELSR-----QLEEKESIVSQLSRSKQFAQTQOTEEL-----KQGLE-EENKAKNALAHAL	1334
Qy	265	ORDRLPQPCREOVVDPRVGGRGFGAGELGQTPQVQAALSYS-----	308
Db	1335	QSSRHDCDLLREQYEEQEQ-----GKAEL-----QRALSKANSEVAQWRKYETDAI	1381
Qy	309	QENPEMGEPRDQLVDPDGOEEBQEA-----AGEGRNQKLARGE-DYNNMDENEABSETD	362
Db	1382	QRTLEELEAAKKKLAQRLQDSEEQVEAVNAKCALEKTKQRLQGEVEDLMYDVERANS---	1438
Qy	363	KQAALAGNDRNID	375
Db	1439	LAALDKKORNF	1451

RESULT 6

```

RES001 6
US-09-949-016-8888
; Sequence 8888, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8888
; LENGTH: 1963
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8888

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Query Match	8.2%;	Score 166.5;	DB 4;	Length 1963;
Best Local Similarity	23.9%;	Pred. No. 5.7e-05;		
Matches	89;	Conservative 61;	Mismatches 154;	Indels 69; Gaps 14;
Qy	40	DLQTRIMEGRVRRAAARGAVELKKNFQGELEKQRBOLDKIQSHNPOLESVNKLYQ	99	
Db	1134	ELQARIEELEEETAEASRAKTRAKQKRSYARELSERLEEAGGVTSTQIE-LNNKRE	1192	
Qy	100	DEKAVLVNNTTG-----ERLIRVQ-----DQLTKLQRTGRQQDVLQFOKNQ	144	
Db	1193	AEPLKLRDLSEATLQHEAMVATLRKXADSVAEIQEDINLQRVQKLEKESEFKLEI	1252	
Qy	145	TNLERKFSYDLQSCINOMKEVKEQCEERIEVTKKGNEAVASRDLSENNDQROOLQALSE	204	
Db	1253	DDLSSSWE-SVSKSKANLEKI CRTLEDQLSEARGKNEE--IQRSLSELITKQSRLOTEAG	1309	
Qy	205	PQPRLOAAGLPHTPEVPOQKGNVLGNSKSTQPPAPSSSEVVLDSKROVEKEETNEIQVNNEEP	264	
Db	1310	ELSR-----QLEEXESIVSQLSRSKQAFTQOTTEL-----KQOLE-EENKAKNALAHAL	1357	
Qy	265	QRDLRLPQERQGVQVDRPVGGRFGAGELGQTPQVQAALSVS-----	308	
Db	1358	QSSRHPCDLLRQEVEEQE-----GKAEI-----QRLSKANSEVAQWRTKYETDAI	1404	
Qy	309	QENPEMEGPERDQLVIPDQGEEBEQEA-----AGEGRNQKLRGE-DYNDMDNEAESETD	362	
Db	1405	QRTLEELAEAKKLAORLQDSEEQVEAVNAKCAKSLKTKQLQGEVEDLMVDVERANS---	1461	
Qy	363	KQAALAGNDRNID	375	

Db 1462 LAAALDKQRNFD 1474

RESULT 7

US-09-866-108A-15754

; Sequence 15754, Application US/09866108A

; Patent No. 6686188

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aemica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 15754

; LENGTH: 1581

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-866-108A-15754

Query Match 8.2%; Score 165.5; DB 4; Length 1581;

Best Local Similarity 22.9%; Pred. No. 5.1e-05;

Matches 96; Conservative 67; Mismatches 151; Indels 105; Gaps 16;

Qy 42 QTRIMEGRVRRRAAAGAVELKKNFQGELEKQREQLDKI-----QSS 86

Db 1126 QTHSKEMESRDEVEEARQSCQKQKQMEVQEEVDKQVLRKRELEGLATLSQV 1185

Qy 87 HNFQLESVNKLQD---EKAVL-----VNNITGRLIRVLQDQI-----123

Db 1186 NRRDFESEKRLKDKLRTKALLADAQLMLDLKNSAPSKRETAIKNQLESEFTCAAAV 1245

Qy 124 ---KTLQRYNGRLQDVLQFQKQNTNLERKFSYDLSQCNOMKEVKEQCEERIEVTKKG 180

Db 1246 KARKAMEVEIDHLQIDDIKAKTALAEQLS-RLQREKNEIQNLEQDQEDNNELMKKH 1304

Qy 181 NEAV--ASRDLSENDRQOQLALS-----EPQRLQAAGLPHTPEVPGKGNVLGNS---K 231

Db 1305 KAAVAQASRDIAQINDLQAQLEANKQELQELQAL-----QSQVEFLEQSMVDK 1356

Qy 232 SQTPAPSEVVLDSKQVE-KEETNEIQVNVNEEPQDRILPQFPGREQVVEDPVGGRGFG 290

Db 1357 SLVSRQEAKEI-----RELFTLEPFTQVRLSLASRLKE--NMKEKLETERD-----1402

Qy 291 GAGELGQTPVQAALSVSQENPEMGPEDQLVTPDQGESEQAAGEGRNQOKLRGEDDY 350

Db 1403 -----QRTAAENREKQNKRLQRLDRTKEEMGELARKEAASRKKHELEM 1448

Qy 351 NWDENEARESET-----DKQAALAG---NDRNIDVFNVEDQKRTDINILLDOR 393

Db 1449 DLESLEAANQSLQADKLAKFKRIGDLQAIEDMESDENEDLINSEGDSDVDSELEDR 1506

RESULT 8

US-08-056-200-94

; Sequence 94, Application US/08056200

; Patent No. 5616500

GENERAL INFORMATION:

; APPLICANT: Steinert, Peter M.

; APPLICANT: Lee, Seung-Chul

; APPLICANT: Kim, In-Gyu

; APPLICANT: Chung, Soo-Il

; APPLICANT: Park, Sang-Chul

; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and

; TITLE OF INVENTION: Methods of Using Same

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/056,200

FILING DATE: 30-APR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fedrick, Michael F.

REGISTRATION NUMBER: 36,799

REFERENCE/DOCKET NUMBER: NIH054.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (714) 760-0404

TELEFAX: (714) 760-9502

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 1898 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-056-200-94

Query Match 8.1%; Score 165; DB 1; Length 1898;

Best Local Similarity 23.2%; Pred. No. 7.3e-05;

Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;

Qy 49 EGRVTRAAAGAVELKKNFQGELEKQREQLDKIQSSHNFQLESVNKLQDEKAVLYNN 108

Db 583 EQLKREOFERRDQLLKREERROQLKREOEERLE--ORLKREVERLEOEER-----634

Qy 109 ITTGERLIRVLQDQ-----LQNTYGRLOQDVLQFQKQNTNLERKFSYD-LSQC 158

Db 635 ---RDERLKREPEERRRHLLKSEQEERHQLARE--QQERRQRLKREERLEQR 690

Qy 159 INQMKVEQCEERIEEVYTKGNEAVASR-----DLSENDRQOQLALSPEQRLQA 212

Db 691 LKREHEERREQLAEAEQEARERIKSRIPKQWQLESEADARQSKVLLAPQ-----A 745

Qy 213 GLPHTVEVPGKGNVLGNSKQTPAPSEVVLDSKQVEKEETNEIQVNVNEEPQDRILPQ- 271

Db 746 G--RAEAFQEQ-----EEKRR-----ESELQWQEEERAHQQQEEQRDFTWQ 789

QY 272 -----EPGRQVVDPRVGGGFGAGELGQTPOVQAALSVSQENPEMEGPERDQVIP 325
DB 790 QAEEKSERGRQRLSARPLREQ-----REQLRAE-----ERQOREQFLP 830
QY 326 DQBEQEQAAGEGRNQ-----QKLRGDDYNNDENEASETDKQAALAGNDRNIDVFNVE 380
DB 831 --EKEEKGQRGRREKELQFLFEEQLQRRARAQQLQBEEDGLQEDQER-----RRQ 883
QY 381 DQKRD---TINLLDQREKRNHTL 400
DB 884 EQRDQKWRWOLEEERKRRHTL 906
RESULT 9
US-08-800-644-94
; Sequence 94, Application US/08800644
; Patent No. 5958752
; GENERAL INFORMATION:
; APPLICANT: Steinert, Peter M.
; APPLICANT: Lee, Seung-Chul
; APPLICANT: Kim, In-Gyu
; APPLICANT: Chung, Soo-Il
; APPLICANT: Park, Sang-Chul
; TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
; TITLE OF INVENTION: Methods of Using Same
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,644
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/056,200
; FILING DATE: 30-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH054.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 760-0404
; TELEFAX: (714) 760-9502
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1898 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-800-644-94
Query Match 8.1%; Score 165; DB 2; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
QY 49 EGRVRAAAARGAVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNN 108
DB 583 EQLKREQEERDQLKKREERQRLKREQEERLE--QRLKREVEERLEQEER-----634
QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLFQKQNTNLKRFSD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLARE--QQRERQRLKREEEERLEQR 690
QY 159 INQMKVEQCEERIEEVTKKGNEAVSR-----DLSENNDQROQLALSEPQLQAA 212
Query Match 8.1%; Score 165; DB 2; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
QY 49 EGRVRAAAARGAVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNN 108
DB 583 EQLKREQEERDQLKKREERQRLKREQEERLE--QRLKREVEERLEQEER-----634
QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLFQKQNTNLKRFSD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLARE--QQRERQRLKREEEERLEQR 690
QY 159 INQMKVEQCEERIEEVTKKGNEAVSR-----DLSENNDQROQLALSEPQLQAA 212

DB 691 LKREHEERERQELAEQEERQARERIKSRIPKQWQLESEADARQSKVLLLEAPQ-----A 745
QY 213 GLPHTFVPGQKGNVLGNSKQTPAPSSVWLDSKQVKEETNEIQVWNEEPQRDLRPO- 271
DB 746 G--RAEAQEQ-----EKKRR-----ESELQWEEERAHFQOQEEERDFTWQW 789
QY 272 -----EPGRQVVDPRVGGGFGAGELGQTPOVQAALSVSQENPEMEGPERDQVIP 325
DB 790 QAEEKSERGRQRLSARPLREQ-----REQLRAE-----ERQOREQFLP 830
QY 326 DQBEQEQAAGEGRNQ-----QKLRGDDYNNDENEASETDKQAALAGNDRNIDVFNVE 380
DB 831 --EKEEKGQRGRREKELQFLFEEQLQRRARAQQLQBEEDGLQEDQER-----RRQ 883
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DB 884 EQRDQKWRWOLEEERKRRHTL 906
RESULT 10
US-09-538-092-1280
; Sequence 1280, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafatSeqformatter Version 0.9
; SEQ ID NO 1280
; LENGTH: 1898
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q07283
US-09-538-092-1280
Query Match 8.1%; Score 165; DB 4; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 90; Gaps 18;
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QY 109 ITTGERLIRVLQDQ-----LKT---LQNYGRLOQDVLFQKQNTNLKRFSD-LSQC 158
DB 635 --RDELKREPEERERHLLKSEQEERHQLARE--QQRERQRLKREEEERLEQR 690
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DB 691 LKREHEERERQELAEQEERQARERIKSRIPKQWQLESEADARQSKVLLLEAPQ-----A 745
QY 213 GLPHTFVPGQKGNVLGNSKQTPAPSSVWLDSKQVKEETNEIQVWNEEPQRDLRPO- 271
DB 746 G--RAEAQEQ-----EKKRR-----ESELQWEEERAHFQOQEEERDFTWQW 789
QY 272 -----EPGRQVVDPRVGGGFGAGELGQTPOVQAALSVSQENPEMEGPERDQVIP 325
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Db 831 --EEEBQGRQRREKELQFLBEEBQLQRRERAQQLBEEBGLQBDQER-----RRQ 883
QY 381 DQKRD---TINLDQREKRNHTL 400
Db 884 EQRDQKWRWQLEERKRRHTL 906

RESULT 11

US-09-538-092-1077
; Sequence 1077, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormatter Version 0.9
; SEQ ID NO 1077
; LENGTH: 1960
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35579
US-09-538-092-1077

Query Match 7.9%; Score 161; DB 4; Length 1960;
Best Local Similarity 21.7%; Pred. No. 0.00017;
Matches 92; Conservative 75; Mismatches 180; Indels 76; Gaps 13;
QY 40 DLOTRIMELEGRVRAAARGAVELKKNFQGELE-----KOREOLDKIQS----- 85
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QY 86 -----SHNFOLESVNKLYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNRLQDDVLQ 139
Db 979 EQIILEDQNCCLAKEKLEEDRIAEFTTNLTTEEESKSLAKLNKHEAMITDLELR 1038
QY 140 FQKQNTNLE---RKFSYDLSCINQMKVEQCEERIEBVTKKGNEAVAS-----RDLS 191
Db 1039 EEKQRELEKTRRKLEGGSTDLSDQIAELQAIABKMLQAKKEBELQAALARVEEAA 1098
QY 192 NNDQROQLQAL---SEQPRLQAGLPHTEVPQK---GNVLGNSKSQ---TPAPSS 240
Db 1099 KNMAKKITRELESQISELQEDLESRSRNKAQKRDLEGELEALKTELEDTLDTAAQ 1158
QY 241 VVLDSKROVE---KEETNEIOVNEEPQDRLPQPGREQVVEDRPVGGRGFGAGELGQ 297
Db 1159 QELSKRQEVNLIKKTLEEAHTHEAQIQEMRQK--HSQAVEEL-----AEQLEQ 1207
QY 298 TPQVOAALSVOENPEME-----GPERDQIVPDGQEEQEAAGEGRNQKLGEDDYNM 353
Db 1208 TKRVKANLEKAKQTLNENRGELANEVKVLQKGDSEHKRKKVEAQLQEL---QVKFNE 1264
QY 354 ENEASETQKQALAGNDRNI-----DVFNVEDQKRTINILDDQREKN 397
Db 1265 EVRVTELADKVTKLQVELDNVTGLLSQSDSKSKLTKDPSALESQLODTQELLQENRQK 1324
QY 398 HTL 400
Db 1325 LSL 1327

RESULT 12

US-09-949-016-10872

; Sequence 10872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10872
; LENGTH: 1960
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10872

Query Match 7.9%; Score 161; DB 4; Length 1960;
Best Local Similarity 21.7%; Pred. No. 0.00017;
Matches 92; Conservative 75; Mismatches 180; Indels 76; Gaps 13;
QY 40 DLOTRIMELEGRVRAAARGAVELKKNFQGELE-----KOREOLDKIQS----- 85
Db 919 DLEARVEEERCOHLQAEKKMQQNIQELBEEQLEESARQKQLEKVTTEAKLKLE 978
QY 86 -----SHNFOLESVNKLYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNRLQDDVLQ 139
Db 979 EQIILEDQNCCLAKEKLEEDRIAEFTTNLTTEEESKSLAKLNKHEAMITDLELR 1038
QY 140 FQKQNTNLE---RKFSYDLSCINQMKVEQCEERIEBVTKKGNEAVAS-----RDLS 191
Db 1039 EEKQRELEKTRRKLEGGSTDLSDQIAELQAIABKMLQAKKEBELQAALARVEEAA 1098
QY 192 NNDQROQLQAL---SEQPRLQAGLPHTEVPQK---GNVLGNSKSQ---TPAPSS 240
Db 1099 KNMAKKITRELESQISELQEDLESRSRNKAQKRDLEGELEALKTELEDTLDTAAQ 1158
QY 241 VVLDSKROVE---KEETNEIOVNEEPQDRLPQPGREQVVEDRPVGGRGFGAGELGQ 297
Db 1159 QELSKRQEVNLIKKTLEEAHTHEAQIQEMRQK--HSQAVEEL-----AEQLEQ 1207
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Db 1208 TKRVKANLEKAKQTLNENRGELANEVKVLQKGDSEHKRKKVEAQLQEL---QVKFNE 1264
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QY 398 HTL 400
Db 1325 LSL 1327

RESULT 13

US-09-538-092-863
; Sequence 863, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01

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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:10:23 ; Search time 147 Seconds
(without alignments)
980.145 Million cell updates/sec

Title: US-10-759-803-2

Perfect score: 2029

Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DKQRTINLLDQREKRNHTL 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599520 seqs, 360203123 residues

Total number of hits satisfying chosen parameters: 1599520.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/FCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2029	100.0	400	14	US-10-205-823-156
2	2029	100.0	400	14	Sequence 156, App
3	2029	100.0	400	16	US-10-177-293-184
4	2029	100.0	400	16	Sequence 184, App
5	2029	100.0	401	10	US-10-759-803-2
6	2029	100.0	401	10	Sequence 2, Appli
7	2029	100.0	401	14	US-09-946-374-100
8	2029	100.0	401	14	Sequence 100, App
9	2029	100.0	401	14	US-10-028-072-486
10	2029	100.0	401	14	Sequence 486, App
11	2029	100.0	401	14	US-10-140-808-486
12	2029	100.0	401	14	Sequence 486, App
13	2029	100.0	401	14	US-10-121-049-486
14	2029	100.0	401	14	Sequence 486, App
15	2029	100.0	401	14	US-10-123-904-486
16	2029	100.0	401	14	Sequence 486, App
17	2029	100.0	401	14	US-10-140-470-486
18	2029	100.0	401	14	Sequence 486, App
19	2029	100.0	401	14	US-10-175-746-486
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23	2029	100.0	401	14	US-10-176-921-486
24	2029	100.0	401	14	Sequence 486, App

13	2029	100.0	401	14	US-10-137-865-486
14	2029	100.0	401	14	Sequence 486, App
15	2029	100.0	401	14	US-10-140-474-486
16	2029	100.0	401	14	Sequence 486, App
17	2029	100.0	401	14	US-10-142-431-486
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19	2029	100.0	401	14	US-10-143-114-486
20	2029	100.0	401	14	Sequence 100, App
21	2029	100.0	401	14	US-10-006-856A-100
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25	2029	100.0	401	14	US-10-123-262-486
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29	2029	100.0	401	14	US-10-006-818A-100
30	2029	100.0	401	14	Sequence 100, App
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33	2029	100.0	401	14	US-10-141-755-486
34	2029	100.0	401	14	Sequence 486, App
35	2029	100.0	401	14	US-10-143-032-486
36	2029	100.0	401	14	Sequence 100, App
37	2029	100.0	401	14	US-10-006-485A-100
38	2029	100.0	401	14	Sequence 486, App
39	2029	100.0	401	14	US-10-013-907A-100
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					Sequence 100, App
					US-10-012-121A-100
					Sequence 486, App
					US-10-124-824-486
					Sequence 486, App
					US-10-127-825A-486
					Sequence 486, App
					US-10-127-829A-486
					Sequence 486, App

ALIGNMENTS

RESULT 1

US-10-205-823-156
; Sequence 156, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-156

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Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120

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Db 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTPAPSS 240

QY 241 VVLDKROVEKEETNEIOVNEEPPORDRLPOEPGREQVVEDRPPVCGRGFGGAGELGQTPQ 300
   |||||
Db 241 VVLDKROVEKEETNEIOVNEEPPORDRLPOEPGREQVVEDRPPVCGRGFGGAGELGQTPQ 300

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   |||||
Db 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQOKLRGEDDYNNDENEASE 360

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400
   |||||
Db 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400

RESULT 2
US-10-177-293-184
; Sequence 184, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jk., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
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; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-184

Query Match      100.0%; Score 2029; DB 14; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSDVLTQTRIMELEGRVRRAAERG 60
   |||||
Db 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSDVLTQTRIMELEGRVRRAAERG 60

QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
   |||||
Db 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120

QY 121 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEEVTKKG 180
   |||||
Db 121 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINOMKEVKEQCEERIEEVTKKG 180

QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTPAPSS 240
   |||||
Db 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTPAPSS 240

QY 241 VVLDKROVEKEETNEIOVNEEPPORDRLPOEPGREQVVEDRPPVCGRGFGGAGELGQTPQ 300
   |||||
Db 241 VVLDKROVEKEETNEIOVNEEPPORDRLPOEPGREQVVEDRPPVCGRGFGGAGELGQTPQ 300

QY 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQOKLRGEDDYNNDENEASE 360
   |||||
Db 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQOKLRGEDDYNNDENEASE 360

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400
   |||||
Db 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNTL 400

RESULT 3
US-10-759-803-2
; Sequence 2, Application US/10759803
; Publication No. US20040265310A1
; GENERAL INFORMATION:
; APPLICANT: AFAR, Daniel E. H.
; APPLICANT: HUBERT, Rene S.
; APPLICANT: LEONG, Kahan
; APPLICANT: RAITANO, Arthur B.
; APPLICANT: SAPPAN, Douglas C.
; TITLE OF INVENTION: NOVEL PROSTATE-RESTRICTED GENE EXPRESSED
; FILE REFERENCE: 129.13USUI
; CURRENT APPLICATION NUMBER: US/10/759,803
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/547,788
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/128,860
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: SIGNAL
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; LOCATION: (1)....(29)
US-10-759-803-2

Query Match      100.0%; Score 2029; DB 16; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLGNRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAABRG 60
Db 1 MGLGNRSMKSPPLVLAALVACIIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAABRG 60

QY 61 AVELKKNFQGELEKQREOLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREOLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120

QY 121 DQKTLQRYNGRLQDVLQFQKNQNTLNRKFSYDLSQINOMKEVKEQCEERIEBVTKKG 180
Db 121 DQKTLQRYNGRLQDVLQFQKNQNTLNRKFSYDLSQINOMKEVKEQCEERIEBVTKKG 180

QY 181 NEAVASRDLSNNDRQQLALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTPAPSE 240
Db 181 NEAVASRDLSNNDRQQLALSEPQRLQAAGLPHTPEVPOQKGNVLGNSKSTPAPSE 240

QY 241 VVLDKROVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 300
Db 241 VVLDKROVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 300

QY 301 VOALSVSQENPEMGPGRDOLVDPGQEEQEAAGEGRNQKLGEDDYNNDENAESE 360
Db 301 VOALSVSQENPEMGPGRDOLVDPGQEEQEAAGEGRNQKLGEDDYNNDENAESE 360

QY 361 TDKQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
Db 361 TDKQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400

RESULT 4
US-09-946-374-100
; Sequence 100, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
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; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
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; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279

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PRIOR FILING DATE: 1998-09-22	PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101473
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103711

[illegible]

; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
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; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-10-24
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; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
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; PRIOR FILING DATE: 1997-10-28
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; PRIOR FILING DATE: 1997-10-29
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; PRIOR APPLICATION NUMBER: 60/069278
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; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
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; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
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; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
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; PRIOR FILING DATE: 1998-04-09
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-12
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
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; PRIOR FILING DATE: 1998-05-22

;
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAAERG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAAERG 61

QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQYDEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQYDEKAVLVNNITTTGERLIRVLQ 121

QY 121 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVKECEERIEEVTKKG 180
DB 122 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVKECEERIEEVTKKG 181

QY 181 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 241

QY 241 VVLDKSRQVKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
DB 242 VVLDKSRQVKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 301

QY 301 VQAAALSVQENPEMGPEDQLVIPDQEEEOAAGEGRNQKLRGEDDYNNDENEABSE 360
DB 302 VQAAALSVQENPEMGPEDQLVIPDQEEEOAAGEGRNQKLRGEDDYNNDENEABSE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401

RESULT 6
US-10-140-808-486
; Sequence 486, Application US/10140808

;
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAAERG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSVDLQTRIMELEGRVRRAAAERG 61

QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQYDEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQYDEKAVLVNNITTTGERLIRVLQ 121

QY 121 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVKECEERIEEVTKKG 180
DB 122 DOLKTLQRYNGRLQODVLQFQKQNTNLERKFSYDLSCINQMKVKECEERIEEVTKKG 181

QY 181 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRLSENNDORQQLQALSEPQRLQAAGLPHTPEVPOGKGNVLGNSKSTPAPSE 241

QY 241 VVLDKSRQVKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
DB 242 VVLDKSRQVKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGGRGFGGAGELGQTPQ 301

QY 301 VQAAALSVQENPEMGPEDQLVIPDQEEEOAAGEGRNQKLRGEDDYNNDENEABSE 360
DB 302 VQAAALSVQENPEMGPEDQLVIPDQEEEOAAGEGRNQKLRGEDDYNNDENEABSE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401

RESULT 7
US-10-121-049-486
; Sequence 486, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61
QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINOMKEVKEOEERIEVTKKG 180
DB 122 DQKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINOMKEVKEOEERIEVTKKG 181
QY 181 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOKGNVGNLSKSTQTPAPSE 240
DB 182 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOKGNVGNLSKSTQTPAPSE 241
QY 241 VVLSKROVEKEETNEIQVWNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 300
DB 242 VVLSKROVEKEETNEIQVWNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 301
QY 301 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGRNQKLGEDDYNNDENEAESE 360
DB 302 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGRNQKLGEDDYNNDENEAESE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401

```

```

RESULT 8
US-10-123-904-486
; Sequence 486, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 61
QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINOMKEVKEOEERIEVTKKG 180
DB 122 DQKTLQRYNGLQDVLQFQKNQTNLERKFSYDLSQCINOMKEVKEOEERIEVTKKG 181
QY 181 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOKGNVGNLSKSTQTPAPSE 240
DB 182 NEAVASRLSENNDQRLQALSEPQRLQAAGLPHTPEVPOKGNVGNLSKSTQTPAPSE 241
QY 241 VVLSKROVEKEETNEIQVWNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 300
DB 242 VVLSKROVEKEETNEIQVWNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 301
QY 301 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGRNQKLGEDDYNNDENEAESE 360
DB 302 VQAAALSVQENPEMGPEDQVLPDGOEEQEAAGEGRNQKLGEDDYNNDENEAESE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401

```

```

RESULT 9
US-10-140-470-486
; Sequence 486, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.

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; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAARG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAARG 61
QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKKG 180
DB 122 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKKG 181
QY 181 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTPEVPOGKGNVLGNSKSTPAPSS 240
DB 182 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTPEVPOGKGNVLGNSKSTPAPSS 241
QY 241 VVLSKQVKEETNEIQVNNEEPORDRLPOPGREQVVEDRPGVGRGFGGAGELGQTPQ 300
DB 242 VVLSKQVKEETNEIQVNNEEPORDRLPOPGREQVVEDRPGVGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPEDQVLIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 360
DB 302 VQAALSVSQENPEMGPEDQVLIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401
```

```
RESULT 10
US-10-175-746-486
; Sequence 486, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-486

Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAARG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRRRAAARG 61
QY 61 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIOSSHNFQLESVNKLQDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKKG 180
DB 122 DQLKTLQRYNRLQODVLQFQKNQTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKKG 181
QY 181 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTPEVPOGKGNVLGNSKSTPAPSS 240
DB 182 NEAVASRLSENNDORQOLQALSEPQRLQAGLPHTPEVPOGKGNVLGNSKSTPAPSS 241
QY 241 VVLSKQVKEETNEIQVNNEEPORDRLPOPGREQVVEDRPGVGRGFGGAGELGQTPQ 300
DB 242 VVLSKQVKEETNEIQVNNEEPORDRLPOPGREQVVEDRPGVGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPEDQVLIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 360
DB 302 VQAALSVSQENPEMGPEDQVLIPDGQEEQEAAGEGRNQKLRGDDYNNDENEARSE 361
QY 361 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 401
```

```
RESULT 11
US-10-176-918-486
; Sequence 486, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
```



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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-486

```

Query Match	100.0%;	Score 2029;	DB 14;	Length 401;
Best Local Similarity	100.0%;	Pred. No. 2.9e-131;		
Matches 400;	Conservative	0;	Mismatches	0; Indels 0;

Qy	1	MGLGNRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLOTRIMELEGRVYRAAAERG	60
Db	2	MGLGNRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLOTRIMELEGRVYRAAAERG	61
Qy	61	AVELKNEFQCELEKOREQLDKIQSSHNFOLESVNKLQDEKAVLVNNITTCERLIRVLQ	120
Db	62	AVELKNEFQCELEKOREQLDKIQSSHNFOLESVNKLQDEKAVLVNNITTCERLIRVLQ	121
Qy	121	DQLKTLQRYNGLQDVLQFQKNQTNLKRKFSYDLSQCINQMKEYKEQCEERIEEVTKKG	180
Db	122	DQLKTLQRYNGLQDVLQFQKNQTNLKRKFSYDLSQCINQMKEYKEQCEERIEEVTKKG	181
Qy	181	NEAVASRDLSENNDORQOLQALSEPQPLQQAAGLPHTTEVPQKGVLNLSKTSQTAPASSE	240
Db	182	NEAVASRDLSENNDORQOLQALSEPQPLQQAAGLPHTTEVPQKGVLNLSKTSQTAPASSE	241
Qy	241	VVLDSKQKQVEKEETNEIOVNNEEPDRDLQPEPGREQVVEDRPUVGGRGFGGAGELGOTPO	300
Db	242	VVLDSKQKQVEKEETNEIOVNNEEPDRDLQPEPGREQVVEDRPUVGGRGFGGAGELGOTPO	301
Qy	301	VQAALSVSQENPEMEGPERDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNMDENEAERSE	360
Db	302	VQAALSVSQENPEMEGPERDQLVIPDGOEEQEAAGEGRNQOKLRGDDYNNMDENEAERSE	361
Qy	361	TDKQAALAGNDRNDIVFNVEQKRDITINLLDQREKRNHTL	400
Db	362	TDKQAALAGNDRNDIVFNVEQKRDITINLLDQREKRNHTL	401

```

RESULT 12
US/10-176-921-486
; Sequence 486, Application US/10176921
; Publication No. US2003027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRAN
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/17
; Prior Filing DATE: 2002-06-20
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapien

```

US-10-176-921-486

Query Match	100.0%	Score 2029;	DB 14;	Length 401;
Best Local Similarity	100.0%;	Pred. No. 2.9e-131;		
Matches 400;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;

Qy	1	MGLNGRRSMKSPPLVLAALVACIIIVLGFNTYWIASSRVDLQTRIMELEGRVRRAAAERG	60
Db	2	MGLNGRRSMKSPPLVLAALVACIIIVLGFNTYWIASSRVDLQTRIMELEGRVRRAAAERG	61
Qy	61	AVELKKNEFQGELEBKQREQLDKIOSSHNFQLESVNVKLQYDEKAVLVNNTTGERLIRVUQ	120
Db	62	AVELKKNEFQGELEBKQREQLDKIOSSHNFQLESVNVKLQYDEKAVLVNNTTGERLIRVUQ	121
Qy	121	DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVKEQCEERIIEVTKKG	180
Db	122	DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVKEQCEERIIEVTKKG	181
Qy	181	NEAVASRDLSNNDRQOLQALSEPQRLQAAGLPHTVEVPQKGVLNGSKSQTPAPSS	240
Db	182	NEAVASRDLSNNDRQOLQALSEPQRLQAAGLPHTVEVPQKGVLNGSKSQTPAPSS	241
Qy	241	VWLDSKQVKEEETNEIQVNEEFQDRQLPQEGREQVVEDRPGVGRFGGAGELGQTPQ	300
Db	242	VWLDSKQVKEEETNEIQVNEEFQDRQLPQEGREQVVEDRPGVGRFGGAGELGQTPQ	301
Qy	301	VQAALSYSQENPEMGEPPERDQLVIPDQGEFEQEAAGEGRNQOKLRGEDDYNNDENEASE	360
Db	302	VQAALSYSQENPEMGEPPERDQLVIPDQGEFEQEAAGEGRNQOKLRGEDDYNNDENEASE	361
Qy	361	TDKQAALAGNDRNTDVFNVEDQKEDTNNLLDQREKRNHTL	400
Db	362	TDKQAALAGNDRNTDVFNVEDQKEDTNNLLDQREKRNHTL	401

```

RESULT 13
US-10-137-865-486
; Sequence 486, Application US/10137865
; Publication No. US20030032155A1
;
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;
; FILE REFERENCE: F3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
;
; NUMBER OF SEQ ID NOS: 550
;
; SEQ ID NO 486
;
; LENGTH: 401
;
; TYPE: PRT
;
; ORGANISM: Homo Sapien
US-10-137-865-486

```

```
Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Query Match      100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKG 180
DB 122 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKG 181
QY 181 NEAVASRDLSNNDRQOLQALSEPQLQAAGLPHTTEVPQKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRDLSNNDRQOLQALSEPQLQAAGLPHTTEVPQKGNVLGNSKSTPAPSE 241
QY 241 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 300
DB 242 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLGEDDYNDNEAESE 360
DB 302 VQAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLGEDDYNDNEAESE 361
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 400
DB 362 TDKQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 401

RESULT 14

US-10-140-474-486
; Sequence 486, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 61

QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKG 180
DB 122 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKG 181
QY 181 NEAVASRDLSNNDRQOLQALSEPQLQAAGLPHTTEVPQKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRDLSNNDRQOLQALSEPQLQAAGLPHTTEVPQKGNVLGNSKSTPAPSE 241
QY 241 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 300
DB 242 VVLDSKQVEKEETNEIQVNEEPQDRDLPOEPGREQVVEDRVPVGGRGFGGAGELGQTPQ 301
QY 301 VQAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLGEDDYNDNEAESE 360
DB 302 VQAALSVSQENPEMGPGRDQVLPDQGEHEQEAAGEGRNQKLGEDDYNDNEAESE 361
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 400
DB 362 TDKQAALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL 401

RESULT 15

US-10-142-431-486
; Sequence 486, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 486
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-486

Query Match 100.0%; Score 2029; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSSVDLQTRIMELEGRVRAAARG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQKTLQRYNRLQODVLQFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKG 180

122	Db	 DQLTKLQRYGRLOQDVLQFKQNTNLERKFSYDLSQCNQWKEVQECERIEVTKG	181
181	Qy	 NEAVASRDLSNNQROQLQALSEFPQPLQOAGLPHTPEVPOCKGNVLGNKSKQTAPASSE	240
182	Db	 NEAVASRDLSNNQROQLQALSEFPQPLQOAGLPHTPEVPOCKGNVLGNKSKQTAPASSE	241
241	Qy	 VVLDSKQKVEKEETNEIOVNVEEPQDRDLPOBPGRQGVVVEDRPGVGRGFGAGELGQTPQ	300
242	Db	 VVLDSKQKVEKEETNEIOVNVEEPQDRDLPOBPGRQGVVVEDRPGVGRGFGAGELGQTPQ	301
301	Qy	 VQAALSVSQENPEMEGPERDQLVTPDGOEEEOEAAAGEGRNQOKLRGEDDYNMDENEASSE	360
302	Db	 VQAALSVSQENPEMEGPERDQLVTPDGOEEEOEAAAGEGRNQOKLRGEDDYNMDENEASSE	361
361	Qy	 TDKQAALAGNDRNTDVNFVEDQKRDITINLLQREKRNHTL	400
362	Db	 TDKQAALAGNDRNTDVNFVEDQKRDITINLLQREKRNHTL	401

Search completed: June 7, 2005, 14:23:40
Job time : 149 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 13:57:30 ; Search time 162 Seconds
(without alignments)
954.964 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DQKRDITNLLDQEKRNHTL 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2029	100.0	400	3	AAB24352 Human pro
2	2029	100.0	400	6	ABR47475 Breast ca
3	2029	100.0	400	7	ADB75332 Prostate
4	2029	100.0	401	3	AAY99368 Human PRO
5	2029	100.0	401	4	AB66117 Protein o
6	2029	100.0	401	4	AAU12414 Human PRO
7	2029	100.0	401	4	AB49770 Amyloid-b
8	2029	100.0	401	4	AB93295 Human pro
9	2029	100.0	401	4	AB88480 Human mem
10	2029	100.0	401	5	ABP65020 Human pro
11	2029	100.0	401	6	AB017858 Novel hum
12	2029	100.0	401	6	ABU81112 Human PRO
13	2029	100.0	401	6	ABU66812 Human PRO
14	2029	100.0	401	6	ABU59893 Novel sec
15	2029	100.0	401	6	ABO25083 Human sec
16	2029	100.0	401	6	ABU67088 Human sec
17	2029	100.0	401	6	ADA46005 Novel hum
18	2029	100.0	401	6	ADA76436 Human PRO
19	2029	100.0	401	6	ADA19086 Human PRO
20	2029	100.0	401	6	ADA61709 Homo sapi
21	2029	100.0	401	6	ADB19494 Novel hum
22	2029	100.0	401	6	ADB28035 Human PRO
23	2029	100.0	401	6	ADA86514 Novel hum
24	2029	100.0	401	6	ADB16078 Human PRO
25	2029	100.0	401	6	ADA47864 Human PRO

26	2029	100.0	401	6	ABO33610 Novel hum
27	2029	100.0	401	6	ADA67659 Human PRO
28	2029	100.0	401	6	ADB30666 Human PRO
29	2029	100.0	401	6	ADA85962 Novel hum
30	2029	100.0	401	6	ADA97174 Human PRO
31	2029	100.0	401	6	ADA79478 Human PRO
32	2029	100.0	401	6	ADA87617 Novel hum
33	2029	100.0	401	6	ADB16819 Human PRO
34	2029	100.0	401	6	ADA91911 Novel hum
35	2029	100.0	401	6	ADB14974 Human PRO
36	2029	100.0	401	6	ADB18935 Novel hum
37	2029	100.0	401	6	ADA94150 Human PRO
38	2029	100.0	401	6	ADB20046 Novel hum
39	2029	100.0	401	6	ADB13358 Human PRO
40	2029	100.0	401	6	ABO43391 Novel hum
41	2029	100.0	401	6	ADA74612 Human PRO
42	2029	100.0	401	6	ADB24845 Human PRO
43	2029	100.0	401	6	ADA82369 Human PRO
44	2029	100.0	401	6	ADA75332 Human PRO
45	2029	100.0	401	6	ADA85410 Novel hum

ALIGNMENTS

RESULT 1
AAB24352
ID AAB24352 standard; protein; 400 AA.
XX AC AAB24352;
XX DT 14-FEB-2001 (first entry)
XX DE Human prostate specific 30P3C8 protein sequence SEQ ID NO:2.
XX KW Human; prostate specific gene; 30P3C8; prostate cancer; diagnosis;
XX KW cytosolic; gene therapy; vaccine; tumour.
XX OS Homo sapiens.
XX PN WO200061610-A2.
XX PD 19-OCT-2000.
XX PF 12-APR-2000; 2000WO-US010218.
XX PR 12-APR-1999; 99US-0128860P.
XX PA (UROG-) UROGENESYS INC.
XX PI Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;
XX DR WPI; 2000-619224/59.
XX DR N-FSDB; AAC64559.
XX PT 30P3C8 polypeptide and polynucleotide used for diagnosing, treating and
XX PS monitoring development of prostate cancer.
XX PS Claim 1; Page 94-95; 99pp; English.

The present sequence is the human prostate specific protein 30P3C8, which is over-expressed in prostate cancer cells. 30P3C8 has cytostatic activity and can be used in vaccines and gene therapy. Methods for detecting the levels of 30P3C8 protein or mRNA in prostate tissue, bone tissue, lymphatic tissue, serum, blood or semen are used for diagnosing the presence of cancer in an individual or dysregulated cell growth e.g. hyperplasia. The cancers which are detected or diagnosed are of the bladder, pancreas, colon, brain, bone, lung, kidney or prostate by using test samples of serum, blood or urine or tissues of the bladder, pancreas, colon, brain, bone, lung, kidney and prostate. 30P3C8 polynucleotide sequences can be used for treating cancers expressing 30P3C8, particularly prostate cancers. Immunogenic portions of 30P3C8 are used in vaccines to inhibit the development of cancer. Anti-30P3C8

CC monoclonal antibodies bind to 30P3C8 and disrupt interactions between
CC 30P3C8 and other proteins e.g. receptors for which 30P3C8 is a ligand.
CC 30P3C8 may be a growth factor or other molecules involved in tumour growth
CC and metastasis and so anti-30P3C8 antibodies may disrupt the homing or
CC invasion or other cancer promoting activities of 30P3C8. The assays are
CC used for detecting, staging and monitoring prostate cancer. The 30P3C8
CC protein or mRNA are used as additional specific markers for detecting
CC prostate cancer and provide a more specific assay than the serum prostate
CC specific antigen (PSA) assay
XX
XX Sequence 400 AA;

Query Match 100.0%; Score 2029; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
Db 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
QY 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEEVTKKG 180
Db 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEEVTKKG 180
QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSTQTPAPSE 240
Db 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSTQTPAPSE 240
QY 241 VVLDKRVQKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
Db 241 VVLDKRVQKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
QY 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDENEASE 360
Db 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDENEASE 360
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400

RESULT 2
ABR47475
ID ABR47475 standard; protein; 400 AA.
AC ABR47475;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:184.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
XX
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.

XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI East RC, Horcobegyl GN, Fuszta L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR N-PSDB; ACC50169.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 184; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 400 AA;
Query Match 100.0%; Score 2029; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
Db 1 MGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAERG 60
QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
Db 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
QY 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEEVTKKG 180
Db 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVKEQCEERIEEVTKKG 180
QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSTQTPAPSE 240
Db 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSTQTPAPSE 240
QY 241 VVLDKRVQKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
Db 241 VVLDKRVQKEETNEIQVNEEPQDRDLPOEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
QY 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDENEASE 360
Db 301 VQAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDENEASE 360
QY 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
Db 361 TDKQAALAGNDRNIDVFNVEDQKRDITINLLDQREKRNHTL 400
RESULT 3
ADB75332
ID ADB75332 standard; protein; 400 AA.
XX
AC ADB75332;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX

KW Prostate; cancer; cytostatic; gene therapy; marker.

OS Homo sapiens.

XX WO2003009814-A2.

XX PD 06-FEB-2003.

XX PF 25-JUL-2002; 2002WO-US023913.

XX PR 25-JUL-2001; 2001US-0307982P.

XX PR 22-AUG-2001; 2001US-0314356P.

XX PR 25-SEP-2001; 2001US-0325020P.

XX PR 12-DEC-2001; 2001US-0341746P.

XX PR 05-MAR-2002; 2002US-0362158P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX PI Hoersh S, Kamatkar S, Wonsey AM, Glatk K, Zhao X, Anderson D;

XX DR WPI; 2003-248033/24.

XX PT New nucleic acid molecule, useful for diagnosing or treating prostate

XX PT cancer.

XX PS Disclosure; SEQ ID NO 156; 99pp; English.

XX CC The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 400 AA;

Query Match		100.0%;	Score 2029;	DB 7;	Length 400;
Best Local Similarity		100.0%;	Pred. No. 5.8e-140;	Mismatches 0;	Gaps 0;
Matches 400;		Conservative 0;	Indels 0;	Gaps 0;	
QY	1	MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRRAAERG	60		
Db	1	MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRRAAERG	60		
QY	61	AVELKKNEFQGLEKQKOROLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ	120		
Db	61	AVELKKNEFQGLEKQKOROLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ	120		
QY	121	DOLKTLQRYNGELODVLOFQKQNTLRKSYDLQSCINOMKEVKEOCEERIEBVTXKG	180		
Db	121	DOLKTLQRYNGELODVLOFQKQNTLRKSYDLQSCINOMKEVKEOCEERIEBVTXKG	180		
QY	181	NEAVASRDLSENNDORQQLALSEPQRLQAAGLPHTPEVPOGKGNVGNKSKQTPAPSSSE	240		
Db	181	NEAVASRDLSENNDORQQLALSEPQRLQAAGLPHTPEVPOGKGNVGNKSKQTPAPSSSE	240		
QY	241	VVLDSKQVKEETNEIQVNEEPQDRLPQBPGRQVVEDPVGGRFGGAGELGQTPQ	300		
Db	241	VVLDSKQVKEETNEIQVNEEPQDRLPQBPGRQVVEDPVGGRFGGAGELGQTPQ	300		
QY	301	VOAALSQVENPEMGPGRDQLVDPGQEEQEAAGEGNQOKLRGEDDYNNDENEAASE	360		
Db	301	VOAALSQVENPEMGPGRDQLVDPGQEEQEAAGEGNQOKLRGEDDYNNDENEAASE	360		

QY 361 TDQAALAGNDRNIDVFNVEDQKQKRDITINLLDQREKRNHTL 400
Db 361 TDQAALAGNDRNIDVFNVEDQKQKRDITINLLDQREKRNHTL 400

RESULT 4

AAAY99368

ID AAY99368 standard; protein; 401 AA.

XX AAY99368;

XX AC AAY99368;

XX DT 08-AUG-2000 (first entry)

XX DE Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.

XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;

XX KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX OS Homo sapiens.

XX PN WO200012708-A2.

XX PD 09-MAR-2000.

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098716P.

XX PR 01-SEP-1998; 98US-0098749P.

XX PR 01-SEP-1998; 98US-0098750P.

XX PR 02-SEP-1998; 98US-0098803P.

XX PR 02-SEP-1998; 98US-0098821P.

XX PR 02-SEP-1998; 98US-0098843P.

XX PR 02-SEP-1998; 98US-0098536P.

XX PR 09-SEP-1998; 98US-009596P.

XX PR 09-SEP-1998; 98US-009598P.

XX PR 09-SEP-1998; 98US-009602P.

XX PR 09-SEP-1998; 98US-009642P.

XX PR 10-SEP-1998; 98US-0099741P.

XX PR 10-SEP-1998; 98US-0099754P.

XX PR 10-SEP-1998; 98US-0099763P.

XX PR 10-SEP-1998; 98US-0099792P.

XX PR 10-SEP-1998; 98US-0099808P.

XX PR 10-SEP-1998; 98US-0099812P.

XX PR 10-SEP-1998; 98US-0099815P.

XX PR 10-SEP-1998; 98US-0099816P.

XX PR 15-SEP-1998; 98US-0100385P.

XX PR 15-SEP-1998; 98US-0100388P.

XX PR 15-SEP-1998; 98US-0100390P.

XX PR 16-SEP-1998; 98US-0100584P.

XX PR 16-SEP-1998; 98US-0100627P.

XX PR 16-SEP-1998; 98US-0100661P.

XX PR 16-SEP-1998; 98US-0100662P.

XX PR 16-SEP-1998; 98US-0100664P.

XX PR 17-SEP-1998; 98US-0100683P.

XX PR 17-SEP-1998; 98US-0100684P.

XX PR 17-SEP-1998; 98US-0100710P.

XX PR 17-SEP-1998; 98US-0100711P.

XX PR 17-SEP-1998; 98US-0100919P.

XX PR 17-SEP-1998; 98US-0100930P.

XX PR 18-SEP-1998; 98US-0100849P.

XX PR 18-SEP-1998; 98US-0101014P.

XX PR 18-SEP-1998; 98US-0101068P.

XX PR 18-SEP-1998; 98US-0101071P.

XX PR 22-SEP-1998; 98US-0101279P.

XX PR 23-SEP-1998; 98US-0101471P.

XX PR 23-SEP-1998; 98US-0101472P.

XX PR 23-SEP-1998; 98US-0101474P.

XX PR 23-SEP-1998; 98US-0101475P.

XX PR 23-SEP-1998; 98US-0101476P.

XX PR 23-SEP-1998; 98US-0101477P.

XX PR 23-SEP-1998; 98US-0101479P.

PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	XX	(GETH)	GENENTECH INC.
PR	24-SEP-1998;	98US-0101916P.	XX	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PR	29-SEP-1998;	98US-0102240P.	XX	WPI; 2000-237871/20.	
PR	29-SEP-1998;	98US-0102240P.	DR	N-PSDB; AAA37050.	
PR	29-SEP-1998;	98US-0102307P.	XX	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
PR	29-SEP-1998;	98US-0102330P.	PT	PRO polypeptides, useful for screening of potential peptide or small	
PR	29-SEP-1998;	98US-0102484P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PR	29-SEP-1998;	98US-0102484P.	XX	Claim 12; Fig 58; 773pp; English.	
PR	30-SEP-1998;	98US-0102484P.	XX	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
PR	30-SEP-1998;	98US-0102487P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The	
PR	30-SEP-1998;	98US-0102570P.	CC	transmembrane and receptor PRO proteins can be used for screening of	
PR	30-SEP-1998;	98US-0102571P.	CC	potential peptide or small molecule inhibitors of the relevant	
PR	01-OCT-1998;	98US-0102684P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
PR	01-OCT-1998;	98US-0102684P.	CC	encoding then have various industrial applications, including uses as	
PR	02-OCT-1998;	98US-0102687P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR	
PR	02-OCT-1998;	98US-0102687P.	CC	primers and hybridisation probes used in the isolation of the PRO	
PR	06-OCT-1998;	98US-0102659P.	CC	polypeptides from the present invention	
PR	06-OCT-1998;	98US-0102659P.	XX	SQ Sequence 401 AA;	
PR	06-OCT-1998;	98US-0103449P.			
PR	07-OCT-1998;	98US-0103314P.			
PR	07-OCT-1998;	98US-0103315P.			
PR	07-OCT-1998;	98US-0103328P.			
PR	07-OCT-1998;	98US-0103395P.			
PR	07-OCT-1998;	98US-0103396P.			
PR	07-OCT-1998;	98US-0103401P.			
PR	08-OCT-1998;	98US-0103633P.			
PR	08-OCT-1998;	98US-0103678P.			
PR	08-OCT-1998;	98US-0103679P.			
PR	08-OCT-1998;	98US-0103711P.			
PR	14-OCT-1998;	98US-0104257P.			
PR	20-OCT-1998;	98US-0104987P.			
PR	20-OCT-1998;	98US-0105000P.			
PR	20-OCT-1998;	98US-0105002P.			
PR	21-OCT-1998;	98US-0105104P.			
PR	22-OCT-1998;	98US-0105169P.			
PR	22-OCT-1998;	98US-0105266P.			
PR	26-OCT-1998;	98US-0105693P.			
PR	26-OCT-1998;	98US-0105694P.			
PR	27-OCT-1998;	98US-0105807P.			
PR	27-OCT-1998;	98US-0105881P.			
PR	27-OCT-1998;	98US-0105882P.			
PR	27-OCT-1998;	98US-0106062P.			
PR	28-OCT-1998;	98US-0106023P.			
PR	28-OCT-1998;	98US-0106029P.			
PR	28-OCT-1998;	98US-0106030P.			
PR	28-OCT-1998;	98US-0106032P.			
PR	28-OCT-1998;	98US-0106033P.			
PR	28-OCT-1998;	98US-0106178P.			
PR	29-OCT-1998;	98US-0106248P.			
PR	29-OCT-1998;	98US-0106384P.			
PR	29-OCT-1998;	98US-0108500P.			
PR	30-OCT-1998;	98US-0108464P.			
PR	03-NOV-1998;	98US-0106856P.			
PR	03-NOV-1998;	98US-0106902P.			
PR	03-NOV-1998;	98US-0106905P.			
PR	03-NOV-1998;	98US-0106919P.			
PR	03-NOV-1998;	98US-0106932P.			
PR	03-NOV-1998;	98US-0106934P.			
PR	10-NOV-1998;	98US-0107783P.			
PR	17-NOV-1998;	98US-0108775P.			
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108867P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
PR	18-NOV-1998;	98US-0108850P.			
PR	18-NOV-1998;	98US-0108851P.			
<hr/>					
PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101743P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	XX	(GETH)	GENENTECH INC.
PR	24-SEP-1998;	98US-0101916P.	XX	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PR	29-SEP-1998;	98US-0102240P.	XX	WPI; 2000-237871/20.	
PR	29-SEP-1998;	98US-0102240P.	DR	N-PSDB; AAA37050.	
PR	29-SEP-1998;	98US-0102307P.	XX	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
PR	29-SEP-1998;	98US-0102330P.	PT	PRO polypeptides, useful for screening of potential peptide or small	
PR	29-SEP-1998;	98US-0102484P.	PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PR	29-SEP-1998;	98US-0102484P.	XX	Claim 12; Fig 58; 773pp; English.	
PR	30-SEP-1998;	98US-0102484P.	XX	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
PR	30-SEP-1998;	98US-0102487P.	CC	receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The	
PR	30-SEP-1998;	98US-0102570P.	CC	transmembrane and receptor PRO proteins can be used for screening of	
PR	30-SEP-1998;	98US-0102571P.	CC	potential peptide or small molecule inhibitors of the relevant	
PR	01-OCT-1998;	98US-0102684P.	CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
PR	01-OCT-1998;	98US-0102684P.	CC	encoding then have various industrial applications, including uses as	
PR	02-OCT-1998;	98US-0102687P.	CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR	
PR	02-OCT-1998;	98US-0102687P.	CC	primers and hybridisation probes used in the isolation of the PRO	
PR	06-OCT-1998;	98US-0102659P.	CC	polypeptides from the present invention	
PR	06-OCT-1998;	98US-0102659P.	XX	SQ Sequence 401 AA;	
PR	07-OCT-1998;	98US-0103314P.			
PR	07-OCT-1998;	98US-0103315P.			
PR	07-OCT-1998;	98US-0103328P.			
PR	07-OCT-1998;	98US-0103395P.			
PR	07-OCT-1998;	98US-0103396P.			
PR	07-OCT-1998;	98US-0103401P.			
PR	08-OCT-1998;	98US-0103633P.			
PR	08-OCT-1998;	98US-0103678P.			
PR	08-OCT-1998;	98US-0103679P.			
PR	08-OCT-1998;	98US-0103711P.			
PR	14-OCT-1998;	98US-0104257P.			
PR	20-OCT-1998;	98US-0104987P.			
PR	20-OCT-1998;	98US-0105000P.			
PR	20-OCT-1998;	98US-0105002P.			
PR	21-OCT-1998;	98US-0105104P.			
PR	22-OCT-1998;	98US-0105169P.			
PR	22-OCT-1998;	98US-0105266P.			
PR	26-OCT-1998;	98US-0105693P.			
PR	26-OCT-1998;	98US-0105694P.			
PR	27-OCT-1998;	98US-0105807P.			
PR	27-OCT-1998;	98US-0105881P.			
PR	27-OCT-1998;	98US-0105882P.			
PR	27-OCT-1998;	98US-0106062P.			
PR	28-OCT-1998;	98US-0106023P.			
PR	28-OCT-1998;	98US-0106029P.			
PR	28-OCT-1998;	98US-0106030P.			
PR	28-OCT-1998;	98US-0106032P.			
PR	28-OCT-1998;	98US-0106033P.			
PR	28-OCT-1998;	98US-0106178P.			
PR	29-OCT-1998;	98US-0106248P.			
PR	29-OCT-1998;	98US-0106384P.			
PR	29-OCT-1998;	98US-0108500P.			
PR	30-OCT-1998;	98US-0108464P.			
PR	03-NOV-1998;	98US-0106856P.			
PR	03-NOV-1998;	98US-0106902P.			
PR	03-NOV-1998;	98US-0106905P.			
PR	03-NOV-1998;	98US-0106919P.			
PR	03-NOV-1998;	98US-0106932P.			
PR	03-NOV-1998;	98US-0106934P.			
PR	10-NOV-1998;	98US-0107783P.			
PR	17-NOV-1998;	98US-0108775P.			
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108867P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
PR	18-NOV-1998;	98US-0108850P.			
PR	18-NOV-1998;	98US-0108851P.			
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Query Match 100.0%; Score 2029; DB 3; Length 401;					
Best Local Similarity 100.0%; Pred. No. 5.8e-140;					
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MGLNGRSMKSPPLVLAALVACIIIVLGFNFWIASSRSVDLQTRIMELEGRVRRAAERG	60		
DB	2	MGLNGRSMKSPPLVLAALVACIIIVLGFNFWIASSRSVDLQTRIMELEGRVRRAAERG	61		
QY	61	AVELKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQDEKAVLVNNITTTGERLIRVLQ	120		
DB	62	AVELKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQDEKAVLVNNITTTGERLIRVLQ	121		
QY	121	DQLKTLQRYGRLOQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG	180		
DB	122	DQLKTLQRYGRLOQDVLQFQKQNTNLERKFSYDLSCINOMKEVKEOCEERIEVTKKG	181		
QY	181	NEAVASRDLSNNDRQQLQALSEPQRLQALPHTTEVPQKGNVLSKSTQTPAPSS	240		
DB	182	NEAVASRDLSNNDRQQLQALSEPQRLQALPHTTEVPQKGNVLSKSTQTPAPSS	241		
QY	241	VVLDSKQVKEETNEIQVWNEEPORDRLPOBPQREQVVEQVVEQVGGFGAGELGQTPQ	300		
DB	242	VVLDSKQVKEETNEIQVWNEEPORDRLPOBPQREQVVEQVVEQVGGFGAGELGQTPQ	301		
QY	301	VOAALSVSQENPEMEGPERDQLVIPDQEEBQEAAGEGRNQOKLRGEDDYNNDENEASE	360		
DB	302	VOAALSVSQENPEMEGPERDQLVIPDQEEBQEAAGEGRNQOKLRGEDDYNNDENEASE	361		
QY	361	TDKQALAGNDRNDIVFNVEDQKRTINLLDQREKRNHTL	400		
DB	362	TDKQALAGNDRNDIVFNVEDQKRTINLLDQREKRNHTL	401		
RESULT 5					
AAB66117					
ID	AAB66117	standard; protein; 401 AA.			
XX					
AC	AAB66117;				
XX					
DT	02-APR-2001	(first entry)			
XX					
DE	Protein of the invention #29.				
XX					
KW	Secreted; transmembrane; gene therapy.				

XX Unidentified.
 XX WO200078961-A1.
 XX PD 28-DEC-2000.
 XX PF 18-FEB-2000; 2000WO-US004342.
 XX PR 23-JUN-1999; 99US-0141037P.
 XX PR 20-JUL-1999; 99US-0144758P.
 XX PR 26-JUL-1999; 99US-0145698P.
 XX PR 01-SEP-1999; 99WO-US020111.
 XX PR 29-OCT-1999; 99US-0162506P.
 XX PR 30-NOV-1999; 99WO-US028313.
 XX PR 02-DEC-1999; 99WO-US028551.
 XX PR 16-DEC-1999; 99WO-US030095.
 XX PR 05-JAN-2000; 2000WO-US000219.
 XX PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2001-071395/08.
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX Claim 1; Fig 58; 787pp; English.
 XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX Sequence 401 AA;
 SQ
 Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140; Indels 0; Gaps 0;
 Matches 400; Conservative 0; Mismatches 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSRVDLQTRIMELEGRVRRRAAERG 60
 Db 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNYWIASRSRVDLQTRIMELEGRVRRRAAERG 61
 QY 61 AVELKKNFQGLEKQREQLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
 Db 62 AVELKKNFQGLEKQREQLDKIQSHNFQLESVKNLYODEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNGRLQDVLQFQKQNTNLRKFSYDLSQCINQMKVEKCEERIEBVTKKG 180
 Db 122 DQKTLQRYNGRLQDVLQFQKQNTNLRKFSYDLSQCINQMKVEKCEERIEBVTKKG 181
 QY 181 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSKTAPASSE 240
 Db 182 NEAVASRLSENDRQQLQALSEPQRLQAAGLPHTTEVPQKGNVLGNSKSKTAPASSE 241
 QY 241 VVLDKRVQKEETNEIQVNEEPQDRILPQPGREQVVEDRPVCGRGFGGAGELGQTPQ 300
 Db 242 VVLDKRVQKEETNEIQVNEEPQDRILPQPGREQVVEDRPVCGRGFGGAGELGQTPQ 301
 QY 301 VQAAALSQENPEMGPGRDQLVPDGOEEQEAAGEGRNQKLRGEDDYNDNEAESE 360
 Db 302 VQAAALSQENPEMGPGRDQLVPDGOEEQEAAGEGRNQKLRGEDDYNDNEAESE 361

QY 361 TDKQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
 ||||||||||||||||||||||||||||||||||||||||
 Db 362 TDKQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401
 ||||||||||||||||||||||||||||||||||||||||
 RESULT 6
 AAU12414
 ID AAU12414 standard; protein; 401 AA.
 XX AAU12414;
 AC AAU12414;
 XX 24-OCT-2001 (first entry)
 DT 24-OCT-2001 (first entry)
 XX Human PRO1326 polypeptide sequence.
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200140466-A2.
 PN 07-JUN-2001.
 PD 01-DEC-2000; 2000WO-US032678.
 PF 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnovers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21486.
 XX
 PT Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 12; Fig 486; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VITA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRAAAERG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRAAAERG 61
 QY 61 AVELKKNFQGELEKQREOLDKIQSSHNFOLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
 DB 62 AVELKKNFQGELEKQREOLDKIQSSHNFOLESVKNLYODEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKG 180
 DB 122 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKG 181
 QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOKGNVLGNSKSTQTPAPSE 240
 DB 182 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOKGNVLGNSKSTQTPAPSE 241
 QY 241 VVLDKRVQKEETNEIOVNVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 300
 DB 242 VVLDKRVQKEETNEIOVNVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 301
 QY 301 VQAAALSVSQENPEMGPGRDQLVDPGQEEQEAAGRNQKLRGEDDYNNDENEAESE 360
 DB 302 VQAAALSVSQENPEMGPGRDQLVDPGQEEQEAAGRNQKLRGEDDYNNDENEAESE 361
 QY 361 TDQQAALAGNDRNIDVFNVEDQKRTDITINLLDQREKRNHTL 400
 DB 362 TDQQAALAGNDRNIDVFNVEDQKRTDITINLLDQREKRNHTL 401

RESULT 7
 AAB49770
 ID AAB49770 standard; protein; 401 AA.
 XX
 AC AAB49770;
 XX

DT 20-APR-2001 (first entry)
 XX
 DE Amyloid-beta protein agglutination regulating factor SEQ ID 8.
 XX
 KW Human; amyloid-beta protein; agglutination regulatory factor;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FN WO200104299-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 06-JUL-2000; 2000WO-JP004515.
 XX
 PR 08-JUL-1999; 99JP-00194179.
 PR 18-OCT-1999; 99US-0159586P.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
 PI Arakawa H, Morita M;
 XX
 DR WPI; 2001-138347/14.
 DR N-PSDB; AAF29360.
 XX
 PT Polynucleotide encoding Amyloid-beta protein agglutination-controlling
 PT factor, useful for inhibiting or promoting agglutination or sedimentation
 PT of amyloid-beta protein and in diagnosis and screening drugs for
 PT Alzheimer's disease.
 XX
 PS Claim 1; Page 56-58; 72pp; Japanese.
 XX
 CC This invention relates to polynucleotides AAF29357 - AAF29361 which
 CC encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
 CC agglutination of amyloid beta protein. The protein and polynucleotide
 CC sequences are useful in the diagnosis of Alzheimer's disease. They are
 CC also useful for screening drugs which are useful for treating Alzheimer's
 CC disease
 XX
 SQ Sequence 401 AA;
 Query Match 100.0%; Score 2029; DB 4; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.8e-140;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRAAAERG 60
 DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASRSVDLQTRIMELEGRVRAAAERG 61
 QY 61 AVELKKNFQGELEKQREOLDKIQSSHNFOLESVKNLYODEKAVLVNNTTGERLIRVLQ 120
 DB 62 AVELKKNFQGELEKQREOLDKIQSSHNFOLESVKNLYODEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKG 180
 DB 122 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKG 181
 QY 181 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOKGNVLGNSKSTQTPAPSE 240
 DB 182 NEAVASRDLSNNDRQQLQALSEPQRLQAAGLPHTPEVPOKGNVLGNSKSTQTPAPSE 241
 QY 241 VVLDKRVQKEETNEIOVNVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 300
 DB 242 VVLDKRVQKEETNEIOVNVNEEPQDRDLPOEPGREQVVEDPVGGRFGGAGELGQTPQ 301
 QY 301 VQAAALSVSQENPEMGPGRDQLVDPGQEEQEAAGRNQKLRGEDDYNNDENEAESE 360
 DB 302 VQAAALSVSQENPEMGPGRDQLVDPGQEEQEAAGRNQKLRGEDDYNNDENEAESE 361
 QY 361 TDQQAALAGNDRNIDVFNVEDQKRTDITINLLDQREKRNHTL 400
 DB 362 TDQQAALAGNDRNIDVFNVEDQKRTDITINLLDQREKRNHTL 401

Db	2	MGLNGRRSMKSPPLVLAAALVACIIVLGFNTWIASRRSVDLQTRIMELEGRVRRRAAARG	61
QY	61	AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNKLYQDEKAVLVNNITTTGERLIRVLQ	120
Db	62	AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNKLYQDEKAVLVNNITTTGERLIRVLQ	121
QY	121	DQLKTLQRYNRYGRLOQDVLFQKQNTNLRKFSYDLSCINQWKEVKECEERIEBVTGKG	180
Db	122	DQLKTLQRYNRYGRLOQDVLFQKQNTNLRKFSYDLSCINQWKEVKECEERIEBVTGKG	181
QY	181	NEAVASRDLSNNDRQOQALSPQPRLOAAGLPHTVPOGKGNVLGNSKSTQTPAPSE	240
Db	182	NEAVASRDLSNNDRQOQALSPQPRLOAAGLPHTVPOGKGNVLGNSKSTQTPAPSE	241
QY	241	VVLDSKRQVEKETNEIQVNVNEEPQDRDLPOEPGRQVVEPRVPGRGFGGAGELGQTPQ	300
Db	242	VVLDSKRQVEKETNEIQVNVNEEPQDRDLPOEPGRQVVEPRVPGRGFGGAGELGQTPQ	301
QY	301	VQAALSVSQENPEWEGPERDQVLPDQGEFEQEAAGEGRNQOKLGEDDYNDNEAESE	360
Db	302	VQAALSVSQENPEWEGPERDQVLPDQGEFEQEAAGEGRNQOKLGEDDYNDNEAESE	361
QY	361	TDKQALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL	400
Db	362	TDKQALAGNDRNIDVFNVEDQKRDITNLLDQREKRNHTL	401
RESULT 9			
AA888480			
ID	AA888480	standard; protein; 401 AA.	
AC	AA888480;		
XX	23-MAY-2001	(first entry)	
DT			
XX		Human membrane or secretory protein clone PSEC0242.	
DE			
XX		Human; secretory protein; membrane protein; vaccine; gene therapy;	
KW		rheumatoid arthritis; diabetes.	
XX			
OS		Homo sapiens.	
XX			
FN	EP1067182-A2.		
XX			
PD	10-JAN-2001.		
XX			
PF	07-JUL-2000; 2000EP-00114090.		
XX			
PR	08-JUL-1999; 99JP-00194179.		
PR	11-JAN-2000; 2000JP-00118775.		
PR	02-MAY-2000; 2000JP-00183766.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
FI	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;		
XX			
DR	WPI; 2001-093989/11.		
XX	N-PSDB; AAF93907.		
XX			
PT	Nucleic acids encoding secretory proteins/membrane proteins, useful in		
PT	gene therapy or as candidate target molecules in drug development.		
XX			
PS	Claim 1; SEQ ID NO 328; 609pp + Sequence Listing; English.		
XX			
CC	This invention relates to nucleic acid sequences AAF93744 - AAF93916		
CC	which encode human secretory or membrane proteins represented by AAF88317		
CC	- AAF88419. Included in the invention are primers AAF93917 - AAF94295 and		
CC	AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the		
CC	invention. The invention also includes methods for the production of		
CC	antibodies directed against the proteins, and cDNA sequences, which can		
CC	be used in vaccines. The polynucleotide sequences can be used in gene		
CC	therapy. The polynucleotide sequences and the proteins they encode may be		
CC	used in the prevention, treatment and diagnosis of diseases associated		

AA893295			
ID	AA893295	standard; protein; 401 AA.	
XX			
AC	AA893295;		
XX			
DT	26-JUN-2001	(first entry)	
XX			
DE		Human protein sequence SEQ ID NO:12357.	
XX			
KW		Human; primer; detection; diagnosis; antisense therapy; gene therapy.	
XX			
OS		Homo sapiens.	
XX			
PN	EP1074617-A2.		
XX			
PD	07-FEB-2001.		
XX			
PF	28-JUL-2000; 2000EP-00116126.		
XX			
PR	29-JUL-1999; 99JP-00248036.		
PR	27-AUG-1999; 99JP-00300253.		
PR	11-JAN-2000; 2000JP-00118776.		
PR	02-MAY-2000; 2000JP-00183767.		
PR	09-JUN-2000; 2000JP-00241899.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
FI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX			
DR	WPI; 2001-318749/34.		
XX			
PT	Primer sets for synthesizing polynucleotides, particularly the 5602 full-		
PT	length cDNAs defined in the specification, and for the detection and/or		
PT	diagnosis of the abnormality of the proteins encoded by the full-length		
PT	cDNAs.		
XX			
PS	Claim 8; SEQ ID NO 12357; 2537pp + Sequence Listing; English.		
XX			
CC	The present invention describes primer sets for synthesizing 5602 full-		
CC	length cDNAs defined in the specification. Where a primer set comprises:		
CC	(a) an oligo-dT primer and an oligonucleotide complementary to the		
CC	complementary strand of a polynucleotide which comprises one of the 5602		
CC	nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in the		
CC	specification. The primer sets can be used in antisense therapy and in		
CC	gene therapy. The primers are useful for synthesizing polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893		
CC	represent human amino acid sequences; and AAH13629 to AAH13632 represent		
CC	oligonucleotides, all of which are used in the exemplification of the		
XX	present invention		
XX			
SQ	Sequence 401 AA;		
Query Match	100.0%; Score 2029; DB 4; Length 401;		
Best Local Similarity	100.0%; Pred. No. 5.8e-140;		
Matches 400; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MGLNGRRSMKSPPLVLAAALVACIIVLGFNTWIASRRSVDLQTRIMELEGRVRRRAAARG	60	

CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 61
QY 61 AVELKKNFQGELEKQREOLDKIQSSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREOLDKIQSSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINQMKVKEQCEERIEVTKKG 180
DB 122 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINQMKVKEQCEERIEVTKKG 181
QY 181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEVPQKGNVGNLSKSTPAPSE 240
DB 182 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEVPQKGNVGNLSKSTPAPSE 241
QY 241 VVLDKSKRQVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 300
DB 242 VVLDKSKRQVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 301
QY 301 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDEAESE 360
DB 302 VQAAALSVSQENPEMGPEDQLVDPGQEEQEAAGEGRNQKLRGDDYNNDEAESE 361
QY 361 TDQKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
DB 362 TDQKQALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 10
ABP65020
ID ABP65020 standard; protein; 401 AA.
XX
AC ABP65020;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human protein SEQ ID 680.
XX
KW Human; expressed sequence tag; EST; haematopoietic disorder;
KW central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective.
XX
OS Homo sapiens.
XX
FN WO200259260-A2.
XX

PD 01-AUG-2002.
XX
XX
PF 16-NOV-2001; 2001WO-US042950.
XX
PR 17-NOV-2000; 2000US-00714936.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AU, Yang Y, Wehrman T, Drmanac RT;
XX WPI; 2002-590824/63.
DR N-PSDB; ABQ99606.
XX
PT New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX
XX Claim 20; SEQ ID NO 680; 394pp; English.
XX
CC The present invention relates to novel human coding sequences (ABQ99268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be
CC used in the field of molecular biology as hybridisation probes, primers
CC for PCR, for chromosome and gene mapping, for the recombinant production
CC of protein, or in generation of anti-sense DNA or RNA. The
CC polynucleotides are useful in diagnostics as expressed sequence tags
CC (ESTs) for identifying expressed genes or for physical mapping of the
CC human genome. The proteins may be used as molecular weight markers, or as
CC nutritional sources or supplements. The proteins may be used to maintain
CC and expand cell population in a totipotent or pluripotential state
CC useful for re-engineering damaged or diseased tissues, transplantation,
CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC polynucleotides and proteins are useful for preventing, treating or
CC ameliorating disorders involving aberrant protein expression or
CC biological activity, e.g. haematopoietic disorders, central/peripheral
CC nervous system diseases, mechanical and traumatic disorders, non-healing
CC wounds, immune deficiencies and disorders, infectious diseases caused by
CC viral, bacterial or fungal infection, autoimmune disorders, allergic
CC reactions and conditions, coagulation disorders, or cancer. The
CC polynucleotide sequences of the invention were assembled from ESTs
CC isolated mainly by sequencing by hybridisation, and in some cases,
CC sequences obtained from one or more public databases. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAARG 61
QY 61 AVELKKNFQGELEKQREOLDKIQSSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREOLDKIQSSHNFQLESVNKLQYDEKAVLVNNTTGERLIRVLQ 121
QY 121 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINQMKVKEQCEERIEVTKKG 180
DB 122 DQKTLQRYNGLQDVLQFQKQNTNLERKFSYDLSQCINQMKVKEQCEERIEVTKKG 181
QY 181 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEVPQKGNVGNLSKSTPAPSE 240
DB 182 NEAVASRLSENNDORQQLALSEPQRLQAAGLPHTVEVPQKGNVGNLSKSTPAPSE 241
QY 241 VVLDKSKRQVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 300
DB 242 VVLDKSKRQVEKETNEIQVNEEPQDRDLPOPGREQVVEDRPVGRGFGGAGELGQTPQ 301

QY 301 VOALSVSOENPEMGPEDQVLPDQGEEOEAAGEGNQOKLRGEDDYNNDENAESE 360
 Db 302 VOALSVSOENPEMGPEDQVLPDQGEEOEAAGEGNQOKLRGEDDYNNDENAESE 361
 QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
 Db 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 11
 ABO17858
 ID ABO17858 standard; protein; 401 AA.
 XX ABO17858;
 AC ABO17858;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO1326.
 XX
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antiidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2003032156-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 06-MAY-2002; 2002US-00140474.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 20-NOV-1998; 98WO-US022992.
 PR 01-DEC-1998; 98WO-US024855.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.

PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031243.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US020231.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001US-00908827.
 PR 18-JUL-2001; 2001WO-US021735.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341980/32.
 DR N-PSDB; ACD24095.

XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 486; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, inhibit the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRSMKSPPLVLAALVACILVGNFYWIASRSVDLQTRIMELEGRVRRRAAERG 60
DB 2 MGLNGRSMKSPPLVLAALVACILVGNFYWIASRSVDLQTRIMELEGRVRRRAAERG 61

QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVKNLYQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSHNFQLESVKNLYQDEKAVLVNNTTGERLIRVLQ 121

QY 121 DQLKTLQRYGRLOQDVLFQKNQNLERKFSYDLSCINQMKEVKECEERIEEVTYKG 180
DB 122 DQLKTLQRYGRLOQDVLFQKNQNLERKFSYDLSCINQMKEVKECEERIEEVTYKG 181

QY 181 NEAVASRDLSENNDORQQLQALSEPQPLQAGLPHTPEVQKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRDLSENNDORQQLQALSEPQPLQAGLPHTPEVQKGNVLGNSKSTPAPSE 241

QY 241 VVLDKRVQKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGRGFGGAGELGQTPQ 300
DB 242 VVLDKRVQKEETNEIQVNEEPQDRLLPQPGREQVVEDRPVGRGFGGAGELGQTPQ 301

QY 301 VQAALSVSQENPEMGPDRQLVIPDGBEEBOEAAEGENQOKLRGDDYNNDENEARSE 360
DB 302 VQAALSVSQENPEMGPDRQLVIPDGBEEBOEAAEGENQOKLRGDDYNNDENEARSE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRTDINLLDQREKRNHTL 401

RESULT 12
ABU81112
ID ABU81112 standard; protein; 401 AA.
XX
AC ABU81112;
XX
DT 23-JUN-2003 (first entry)

XX Human PRO polypeptide #243.
DE
XX
KW Human: PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS Homo sapiens.
XX
XX US2003004311-A1.
XX
PD 02-JAN-2003.
XX
XX 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 18-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 31-MAR-1998; 98US-0079728P.
PR 12-JUN-1998; 98US-0080165P.
PR 14-JUL-1998; 98WO-US012456.
PR 28-AUG-1998; 98WO-US014552.
PR 10-SEP-1998; 98WO-US017888.
PR 98WO-US018824.

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PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028554.
PR 02-DEC-1999; 98WO-US028555.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX N-PSDB; ACA67236.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
XX arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
XX heart attack.
XX
XX Claim 12; Fig 486; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the treatment of diabetes, bone and/or cartilage disorders
XX (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
XX hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
XX (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
XX assays for PRO, by detecting its expression in specific cells, tissues or
XX serum, and for affinity purification of PRO from recombinant cell culture
XX or natural sources. ABU80870-ABU81144 represent the human PRO
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CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipadIDEntry.html
XX
XX SQ Sequence 401 AA;
XX
XX Query Match 100.0%; Score 2029; DB 6; Length 401;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-140;
XX Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MGLNGRRSMKSPPLVLAALVACIIIVLGFNFWIASSRVDLQTRIMELEGRRVRAAARG 60
XX DB 2 MGLNGRRSMKSPPLVLAALVACIIIVLGFNFWIASSRVDLQTRIMELEGRRVRAAARG 61
XX
XX QY 61 AVELKQNEFQGELEKQREQLDKIOSSHNFQLESYNKLYQDEKAVLVNNTTGERLIRVLQ 120
XX DB 62 AVELKQNEFQGELEKQREQLDKIOSSHNFQLESYNKLYQDEKAVLVNNTTGERLIRVLQ 121
XX
XX QY 121 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTYKG 180
XX DB 122 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKQCEERIEBVTYKG 181
XX
XX QY 181 NEAVASRDLSNNDRQQLQALSEPPRLQAAGLPHTPEVPGQKGNVLGNSKSTQTPAPSE 240
XX DB 182 NEAVASRDLSNNDRQQLQALSEPPRLQAAGLPHTPEVPGQKGNVLGNSKSTQTPAPSE 241
XX
XX QY 241 VVLDSKQVEKEETNEIQVNVNEEPQRDLPOEPGREQVVEDRPGGRFGGAGELGQTPQ 300
XX DB 242 VVLDSKQVEKEETNEIQVNVNEEPQRDLPOEPGREQVVEDRPGGRFGGAGELGQTPQ 301
XX
XX QY 301 VQAALSVSQENPENMEGPERDQLVIPDQGEERQEAAGEGRNQOKLGEDDYNDENEAESE 360
XX DB 302 VQAALSVSQENPENMEGPERDQLVIPDQGEERQEAAGEGRNQOKLGEDDYNDENEAESE 361
XX
XX QY 361 TDQAALAGNDRNIDVFNVEDQKEDTINLLDQREKRNHTL 400
XX DB 362 TDQAALAGNDRNIDVFNVEDQKEDTINLLDQREKRNHTL 401
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XX RESULT 13
XX ABU66812 standard; protein; 401 AA.
XX AC ABU66812;
XX XX
XX DT 23-MAY-2003 (first entry)
XX
XX DE Human PRO polypeptide #243.
XX
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
XX KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
XX OS Homo sapiens.
XX
XX FN US2003036180-A1.
XX
XX PD 20-FEB-2003.
XX
XX PF 09-MAY-2002; 2002US-00143114.
XX
XX PR 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 14-SEP-1998; 98WO-US019094.
XX PR 14-SEP-1998; 98WO-US019177.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 07-OCT-1998; 98WO-US021141.
XX PR 29-OCT-1998; 98WO-US022991.
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PR	29-OCT-1998;	98WO-US022992.	PR	01-JUN-2001;	2001WO-US017800.
PR	20-NOV-1998;	98WO-US024855.	PR	05-JUN-2001;	2001US-00874503.
PR	01-DEC-1998;	98WO-US025108.	PR	14-JUN-2001;	2001US-00882636.
PR	05-JAN-1999;	99WO-US000106.	PR	19-JUN-2001;	2001US-00886342.
PR	08-MAR-1999;	99WO-US005028.	PR	20-JUN-2001;	2001WO-US019692.
PR	10-MAR-1999;	99WO-US005190.	PR	21-JUN-2001;	2001US-00887879.
PR	20-APR-1999;	99WO-US008615.	PR	22-JUN-2001;	2001WO-US020116.
PR	14-MAY-1999;	99WO-US010733.	PR	29-JUN-2001;	2001WO-US021066.
PR	02-JUN-1999;	99WO-US012252.	PR	09-JUL-2001;	2001WO-US021735.
PR	01-SEP-1999;	99WO-US020111.	PR	18-JUL-2001;	2001US-00908827.
PR	08-SEP-1999;	99WO-US020594.	PR	06-AUG-2001;	2001US-00924419.
PR	13-SEP-1999;	99WO-US020944.	PR	09-AUG-2001;	2001US-00927796.
PR	15-SEP-1999;	99WO-US021090.	PR	16-AUG-2001;	2001US-00931836.
PR	01-DEC-1999;	99WO-US021547.	PR	19-DEC-2001;	2001US-00028072.
PR	15-SEP-1999;	99WO-US021547.	XX		
PR	05-OCT-1999;	99WO-US023089.	PA	(GETH) GENENTECH INC.	
PR	29-NOV-1999;	99WO-US028214.	XX		
PR	30-NOV-1999;	99WO-US028313.	XX		
PR	30-NOV-1999;	99WO-US028409.	PI	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;	
PR	01-DEC-1999;	99WO-US028301.	PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	
PR	01-DEC-1999;	99WO-US028634.	PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
PR	02-DEC-1999;	99WO-US028551.	XX		
PR	02-DEC-1999;	99WO-US028551.	XX		
PR	02-DEC-1999;	99WO-US028554.	DR	WPI; 2003-332040/31.	
PR	02-DEC-1999;	99WO-US028565.	DR	N-FSDB; ACR03845.	
PR	16-DEC-1999;	99WO-US030095.	XX		
PR	20-DEC-1999;	99WO-US030911.	PT	New secreted and transmembrane PRO nucleic acids, useful for gene	
PR	20-DEC-1999;	99WO-US030999.	PT	therapy, in chromosome and gene mapping, as chromosome markers, in tissue	
PR	22-DEC-1999;	99WO-US030720.	PT	typing, and in chromosome identification.	
PR	30-DEC-1999;	99WO-US031243.	XX		
PR	30-DEC-1999;	99WO-US031274.	PS	Claim 12; Fig 486; 660pp; English.	
PR	05-JAN-2000;	2000WO-US000219.	XX		
PR	06-JAN-2000;	2000WO-US000277.	CC	The present invention relates to the isolation of novel human PRO	
PR	06-JAN-2000;	2000WO-US000376.	CC	polypeptides, and the polynucleotide sequences encoding them. The PRO	
PR	11-FEB-2000;	2000WO-US000365.	CC	polypeptides are secreted and transmembrane proteins. The PRO	
PR	18-FEB-2000;	2000WO-US004341.	CC	polypeptides are useful for detecting other PRO polypeptides, for linking	
PR	18-FEB-2000;	2000WO-US004342.	CC	bioactive molecules to cells expressing PRO polypeptides, for modulating	
PR	22-FEB-2000;	2000WO-US004414.	CC	biological activities of cells expressing PRO polypeptides, and for	
PR	24-FEB-2000;	2000WO-US004914.	CC	identifying agonists or antagonists. The PRO polypeptides are useful for	
PR	24-FEB-2000;	2000WO-US005004.	CC	stimulating the release of tumour necrosis factor (TNF)-alpha from	
PR	01-MAR-2000;	2000WO-US005601.	CC	human blood, for stimulating the proliferation or differentiation of	
PR	02-MAR-2000;	2000WO-US005746.	CC	chondrocytes, and detecting the presence of tumours. The polynucleotide	
PR	02-MAR-2000;	2000WO-US005841.	CC	sequences encoding PRO polypeptides are useful as hybridisation probes,	
PR	10-MAR-2000;	2000WO-US006319.	CC	in chromosome and gene mapping, in the generation of antisense RNA and	
PR	15-MAR-2000;	2000WO-US006884.	CC	DNA, in the preparation of PRO polypeptides, for generating transgenic	
PR	20-MAR-2000;	2000WO-US007377.	CC	animals or knockout animals, for the genetic analysis of individuals with	
PR	21-MAR-2000;	2000WO-US007532.	CC	genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the	
PR	30-MAR-2000;	2000WO-US008439.	CC	human PRO polypeptides of the invention. Note: The sequence data for this	
PR	17-MAY-2000;	2000WO-US013705.	CC	patent was obtained in electronic format directly from the USPTO web site	
PR	22-MAY-2000;	2000WO-US014042.	CC	at seqdata.uspto.gov/psipdsIDentry.html	
PR	30-MAY-2000;	2000WO-US014941.	XX		
PR	02-JUN-2000;	2000WO-US015264.	SQ	Sequence 401 AA;	
PR	28-JUL-2000;	2000WO-US020710.		Query Match 100.0%; Score 2029; DB 6; Length 401;	
PR	11-AUG-2000;	2000WO-US022031.		Best Local Similarity 100.0%; Pred. No. 5.8e-140;	
PR	23-AUG-2000;	2000WO-US023522.		Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	24-AUG-2000;	2000WO-US023328.			
PR	08-NOV-2000;	2000WO-US030952.	QY	1 MGLNGRSMKSPPLVLAALVACIIIVLGFNTWYIASSRSVDLQTRIMELEGRVRAAAERG 60	
PR	10-NOV-2000;	2000WO-US030873.			
PR	01-DEC-2000;	2000WO-US032678.	Db	2 MGLNGRSMKSPPLVLAALVACIIIVLGFNTWYIASSRSVDLQTRIMELEGRVRAAAERG 61	
PR	20-DEC-2000;	2000US-00747259.			
PR	20-DEC-2000;	2000WO-US034956.			
PR	28-FEB-2001;	2001US-00796498.	QY	61 AVELKKNFQGELEKQREQLDKIQSSHNFQLESVVKLYQDEKAVLVNNTTGERLIRVLQ 120	
PR	28-FEB-2001;	2001WO-US006520.			
PR	01-MAR-2001;	2001WO-US006666.	Db	62 AVELKKNFQGELEKQREQLDKIQSSHNFQLESVVKLYQDEKAVLVNNTTGERLIRVLQ 121	
PR	09-MAR-2001;	2001US-00802706.			
PR	14-MAR-2001;	2001US-00808689.	QY	121 DOLKTLQRYNGLQODVLQFOKQNTNLERKFSYDLSCINOMKVEKCEERIEEVTYKKG 180	
PR	22-MAR-2001;	2001US-00816744.			
PR	05-APR-2001;	2001US-00828366.	Db	122 DOLKTLQRYNGLQODVLQFOKQNTNLERKFSYDLSCINOMKVEKCEERIEEVTYKKG 181	
PR	10-MAY-2001;	2001US-00854208.			
PR	10-MAY-2001;	2001US-00854280.	QY	181 NEAVASRDLSNNDRQQLALSEPQPRLOAGLPHTPEVPOGKGNVLGNKSKSQTPAPSE 240	
PR	18-MAY-2001;	2001US-00860216.			
PR	25-MAY-2001;	2001US-00866028.	Db	182 NEAVASRDLSNNDRQQLALSEPQPRLOAGLPHTPEVPOGKGNVLGNKSKSQTPAPSE 241	
PR	25-MAY-2001;	2001US-00866034.			
PR	25-MAY-2001;	2001WO-US017092.	QY	241 VVLDKROVEKETWETWIEIOWNEEPDRLPOBPGREOVVEDPVGGRGGGELGQTPQ 300	
PR	01-JUN-2001;	2001US-00872035.			

Db 242 VVLSKROVEKETNEIQVNEEPQDRLLPQEPGCHQVVEDPVGGRGGAGELGQTPQ 301
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Db 302 VQAALSVSQENPEMGPDRQLVDPGQEEQEAAGRGNNQKLRGDDYNNDENEASE 361
QY 361 TDQAALAGNDRNIDVFNVEDOKRDTINLLDQREKRNHTL 400
Db 362 TDQAALAGNDRNIDVFNVEDOKRDTINLLDQREKRNHTL 401

RESULT 14
ABUS9893
ID ABUS9893 standard; protein; 401 AA.
XX
AC ABUS9893;
XX
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1326.
XX
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
XX US2003017563-A1.
PN
XX
PD 23-JAN-2003.
XX
PF
XX 07-MAY-2002; 2002US-00140808.
XX
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025106.
PR 05-JAN-1999; 99WO-US000108.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US007532.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI; 2003-148238/14.
XX N-PSDB; ABX89383.
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX
PS Claim 12; Fig 486; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.8e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRSMKSPPLVLAALVACIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG 60
DB 2 MGLNGRSMKSPPLVLAALVACIIVLGNFYWIASRSVDLQTRIMELEGRVRRAAERG 61

QY 61 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREQLDKIQSHNFQLESVNKLYQDEKAVLVNNTTGERLIRVLQ 121

QY 121 DQKLTQRNYGRLOQDVLFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEBVTKG 180
DB 122 DQKLTQRNYGRLOQDVLFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEBVTKG 181

QY 181 NEAVASRDISENDORQQLQALSEPPQLQAAGLPHTVEPQCKGNVLGNSKQTPAPSE 240
DB 182 NEAVASRDISENDORQQLQALSEPPQLQAAGLPHTVEPQCKGNVLGNSKQTPAPSE 241

QY 241 VVLDKQVKEKETNEIQVNEEPQDRLPQFGREQVVEDPVGGRFGGAGELGQTPQ 300
DB 242 VVLDKQVKEKETNEIQVNEEPQDRLPQFGREQVVEDPVGGRFGGAGELGQTPQ 301

QY 301 VQAALSVSQENPEMGPEDQLVI PDQBEQEAAAGEGRNQKLRGEDDYNMENEASE 360
DB 302 VQAALSVSQENPEMGPEDQLVI PDQBEQEAAAGEGRNQKLRGEDDYNMENEASE 361

QY 361 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 400
DB 362 TDQQAALAGNDRNIDVFNVEDQKRTINLLDQREKRNHTL 401

RESULT 15
ABO25083
ID ABO25083 standard; protein; 401 AA.
XX
AC ABO25083;
XX
DT 05-SEP-2003 (first entry)
XX
XX Human secreted/transmembrane protein (PRO) #243.
XX
XX Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW PBMG; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell; A-peptide; factor VIIA.
XX
OS Homo sapiens.
XX
PN US2003036179-A1.
XX
PD 20-FEB-2003.
XX
PF 10-MAY-2002; 2002US-00142431.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 02-JUN-1999; 99WO-US010733.
PR 01-SEP-1999; 99WO-US012252.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-466355/44.
DR N-PSDB; ACD42037.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 12; Fig 486; 659pb; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 80%
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC extracellular domain (with or without its associated signal peptide),

CC which comprises any of the 275 120-850 residue amino acid sequences,
CC given in the specification; (b) comprising any of the 275 300-3500
CC nucleotide sequences, given in the specification; or (c) comprising the
CC full-length coding sequence of the nucleotide sequences given in the
CC specification, or of the DNA deposited under any of the American Type
CC Culture Collection (ATCC) Accession Numbers listed in the specification.
CC Also included are a vector comprising the novel nucleic acid, a host cell
CC comprising the vector, producing a PRO polypeptide, the isolated PRO
CC polypeptides detailed above, a chimeric molecule comprising the PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO polypeptide in a sample suspected of containing
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulating at least one biological activity of a cell
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC modulating the uptake of glucose or FFA by skeletal muscle cells or
CC adipocyte cells, stimulating the proliferation or differentiation of
CC chondrocyte cells (or proliferation of or gene expression in pericyte
CC cells), stimulating the proliferation of inner ear utricular supporting
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
CC cells, detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences given
CC in the specification. The polynucleotide is useful in molecular biology,
CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence represents a PRO
CC polypeptide
XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2029; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.9e-140;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSSVDLQTRIMELEGRVRAAARG 60
DB 2 MGLNGRRSMKSPPLVLAALVACIIVLGFNTWIASRSSVDLQTRIMELEGRVRAAARG 61
QY 61 AVELKKNFQGELEKQREOLDKIOSSHNFQLESYNKLYODEKAVLVNNITTTGERLIRVLQ 120
DB 62 AVELKKNFQGELEKQREOLDKIOSSHNFQLESYNKLYODEKAVLVNNITTTGERLIRVLQ 121
QY 121 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKCEERIEBVTKKG 180
DB 122 DQLKTLQRYGRLOQDVLFQKQNTNLERKFSYDLSCINQMKVEKCEERIEBVTKKG 181
QY 181 NEAVASRLSENDRQOLQALSEPQRLQAGLPHTVEVPQCKGNVLGNSKSTPAPSE 240
DB 182 NEAVASRLSENDRQOLQALSEPQRLQAGLPHTVEVPQCKGNVLGNSKSTPAPSE 241
QY 241 VVLDKQVEKEETNEIQVNVNEEPQRLPOEGREOVVEDRPGGCGGAGELGQTPQ 300
DB 242 VVLDKQVEKEETNEIQVNVNEEPQRLPOEGREOVVEDRPGGCGGAGELGQTPQ 301
QY 301 VQAALVSQENPEMEGPERDQVLPDGOEEFEQEAAGEGRNQKLGEDDYNNDENAESE 360
DB 302 VQAALVSQENPEMEGPERDQVLPDGOEEFEQEAAGEGRNQKLGEDDYNNDENAESE 361
QY 361 TDQAAALAGNDRNDIVFNVEDQKRDITINLLDQREKRNHTL 400
DB 362 TDQAAALAGNDRNDIVFNVEDQKRDITINLLDQREKRNHTL 401

Search completed: June 7, 2005, 14:10:15
Job time : 165 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 13:57:30 ; Search time 170 Seconds
(without alignments)
1204.892 Million cell updates/sec

Title: US-10-759-803-2

Perfect score: 2029

Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DKRDTNLLDQREKRNHTL 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2029	100.0	401	1 GP73_HUMAN	Q8nbj4 homo sapien
2	1196.5	59.0	393	1 GP73_MOUSE	Q91xa2 mus musculus
3	423	20.8	411	2 Q7ZUC8	Q7zuc8 brachydanio
4	419	20.7	410	2 Q6P0H0	Q6p0h0 brachydanio
5	416.5	20.5	355	2 Q641D4	Q641d4 xenopus lae
6	351.5	17.3	433	2 Q6P4E1	Q6p4e1 homo sapien
7	348	17.2	402	2 Q6RZW6	Q6rzw6 mus musculus
8	345.5	17.0	435	2 Q6P2L7	Q6p2l7 mus musculus
9	324	16.0	380	2 Q6UY45	Q6uy45 homo sapien
10	312	15.4	319	2 Q6RZW5	Q6rzw5 mus musculus
11	255	12.6	176	2 Q8C4Z2	Q8c4z2 mus musculus
12	241	11.9	356	2 Q7T0X8	Q7t0x8 xenopus lae
13	235	11.6	177	2 Q96EM1	Q96em1 homo sapien
14	200.5	9.9	1927	2 Q25142	Q25142 halocynthia
15	185.5	9.1	1491	2 Q75UE0	Q75ue0 lampetra ja
16	185.5	9.1	1934	2 Q75UE1	Q75ue1 lampetra ja
17	185	9.1	1934	2 Q21000	Q21000 caenorhabdi
18	184.5	9.1	1302	2 Q695C7	Q695c7 homo sapien
19	181	8.9	995	2 Q7RT39	Q7rt39 plasmodium
20	180	8.9	1332	2 Q8BQ39	Q8bq39 mus musculus
21	180	8.9	1432	2 Q7Q112	Q7q112 anopheles g
22	180	8.9	1491	2 Q7S473	Q7s473 neurospora
23	178.5	8.8	1966	1 MYSB_CABEL	P02566 caenorhabdi
24	176.5	8.7	1018	2 Q7PF85	Q7pf85 anopheles g
25	176.5	8.7	1047	2 Q9C0B4	Q9c0b4 homo sapien
26	176.5	8.7	1302	2 Q7Z2L3	Q7z2l3 homo sapien
27	176	8.7	1200	2 Q73340	P73340 synechocyst
28	176	8.7	3498	2 Q20497	Q20497 caenorhabdi
29	175.5	8.6	1451	2 Q812D8	Q812d8 plasmodium
30	175.5	8.6	1935	2 Q44934	Q44934 loligo peal
31	175	8.6	1941	2 Q26079	Q26079 placopecten

RESULT 1

GP73_HUMAN
ID GP73_HUMAN STANDARD; PRT; 401 AA.
AC Q8NBj4; Q6IAF4; Q9NRB9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Golgi phosphoprotein 2 (Golgi membrane protein GP73) (UNQ686/PRO1326).
GN Name=GOLPH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE INITIATION, GLYCOSYLATION, TISSUE
SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Liver;
RX MEDLINE=20293047; PubMed=10831838; DOI=10.1016/S0378-1119(00)00136-0;
RA Kladney R.D., Bulla G.A., Guo L., Mason A.L., Tollefson A.E.,
Simon D.J., Koutoubi Z., Fimmel C.J.,
"GP73, a novel Golgi-localized protein upregulated in viral
infection";
RL Gene 249:53-65(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayaashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
Omura Y., Abe K., Kamiyama K., Katsuma N., Sato K., Tanikawa M.,
Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotta Y.,
Kusano J., Togawa K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
Nomura Y., Togawa S., Komai F., Hara R., Takeuchi K., Arita M.,
Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

ALIGNMENTS

32 174.5 8.6 1197 1 CING_HUMAN
33 174 8.6 1738 2 Q76329
34 173 8.5 1992 2 Q80ZB6
35 173 8.5 2000 2 Q6URW6
36 172.5 8.5 1175 2 Q9TY21
37 172.5 8.5 1201 2 Q18392
38 172.5 8.5 1936 2 Q8INZ9
39 172.5 8.5 1936 2 Q8IP00
40 172.5 8.5 1936 2 Q8IP01
41 172.5 8.5 1958 2 Q96062
42 172.5 8.5 1962 1 MYSB_DROME
43 172.5 8.5 1962 2 Q8IP02
44 172.5 8.5 1993 2 Q7PF91
45 172.5 8.5 2016 2 Q7PF90

RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sedhagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RT "Cloning of human full open reading frames in Gateway(TM) system entry
 RT vector (pDONR201).";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SUBCELLULAR LOCATION.
 RX PubMed=12191016;
 RA Puri S., Bachert C., Fimmel C.J., Linstedt A.D.;
 RT "Cycling of early Golgi proteins via the cell surface and endosomes
 RT upon luminal pH disruption.";
 RL Traffic 3:641-653 (2002).
 RN [7]
 RP TISSUE SPECIFICITY.
 RX PubMed=12029628; DOI=10.1053/jhep.2002.32525;
 RA Kladney R.D., Cui X., Bulla G.A., Brunt E.M., Fimmel C.J.;
 RT "Expression of GP73, a resident Golgi membrane protein, in viral and
 RT nonviral liver disease.";
 RL Hepatology 35:1431-1440 (2002).
 RN [8]
 RP INDUCTION BY VIRAL INFECTION.
 RX PubMed=12359426; DOI=10.1006/viro.2002.1523;
 RA Kladney R.D., Tolleson A.E., Wold W.S., Fimmel C.J.;
 RT "Upregulation of the Golgi protein GP73 by adenovirus infection
 RT requires the E1A CtpB interaction domain.";
 RL Virology 301:236-246 (2002).
 CC -!- FUNCTION: Unknown. Cellular response protein to viral infection.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Early Golgi.
 CC Cycles via the cell surface and endosomes upon luminal pH

CC disruption.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
 CC alternative initiation at Met-1 and Met-11;
 CC TISSUE SPECIFICITY: Widely expressed. Highly expressed in colon,
 CC prostate, trachea and stomach. Expressed at lower level in testis,
 CC muscle, lymphoid tissues, white blood cells and spleen.
 CC Predominantly expressed by cells of the epithelial lineage.
 CC Expressed at low level in normal liver. Expression significantly
 CC increased in virus (HBV, HCV) infected liver. Expression does not
 CC increase in liver disease due to non-viral causes (alcohol-induced
 CC liver disease, autoimmune hepatitis). Increased expression in
 CC hepatocytes appears to be a general feature of advanced liver
 CC disease. In liver tissue from patients with adult giant-cell
 CC hepatitis (GCH), it is strongly expressed in hepatocyte-derived
 CC epithelial giant cells. Constitutively expressed by biliary
 CC epithelial cells but not by hepatocytes.
 CC -!- INDUCTION: Up-regulated in response to viral infection. Induced by
 CC the E1A adenoviral protein.
 CC -!- PTM: Glycosylated.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF236056; AAF44663.1; -
 CC EMBL; AK075542; BAC11685.1; -
 CC EMBL; AY358593; AAC89856.1; -
 CC EMBL; CR457201; CAG33482.1; -
 CC EMBL; BC001740; AA001740.1; -
 CC Genew; HGNC:15451; GOLPH2.
 CC MIM; 606804; -
 CC GO; GO:0005794; C:Golgi apparatus; TAS.
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC Alternative initiation; Coiled coil; Glycoprotein; Golgi stack;
 KW Signal-anchor; Transmembrane.
 FT CHAIN 1 401
 FT INIT MET 11 401 Golgi phosphoprotein 2, isoform 1.
 FT DOWAIN 1 11 For isoform 2.
 FT TRANSMEM 13 35 Cytoplasmic (Potential).
 FT SIGNAL-ANCHOR 13 35 Signal-anchor for type II membrane
 FT protein (Potential).
 FT DOMAIN 36 401 Luminal (Potential).
 FT DOMAIN 40 205 Coiled coil (Potential).
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 398 398 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 249 249 Q -> R (in Ref. 4).
 SQ SEQUENCE 401 AA; 45333 MW; 24C1DC31B47B5B77 CRC64;
 Query Match 100.0%; Score 2029; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2e-88;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 60
 Db 2 MGLNGRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRAAARG 61
 QY 61 AVELKKNFQCELEKQREQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ 120
 Db 62 AVELKKNFQCELEKQREQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQ 121
 QY 121 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSSQINQMKVEKQCEERIEEVTKKG 180
 Db 122 DQKTLQRYNGRLQDVLQFQKNQTNLERKFSYDLSSQINQMKVEKQCEERIEEVTKKG 181
 QY 181 NEAVASRLSENNDQROQLQALSEPQRLQAAGLPHTPEVPGKGNVLGNLSKQTPAPSS 240

Db 182 NEAVASRLSENNDRQQQLAUSEPQRLQAAGLPHTEVPQKGNVLGNSKSTQTPAPSE 241
QY 241 VVLDKQVKEKETNEIQVNEEPQDRLPQBPQREQVVEDRVPVGRGFGGAGELGQTPQ 300
Db 242 VVLDKQVKEKETNEIQVNEEPQDRLPQBPQREQVVEDRVPVGRGFGGAGELGQTPQ 301
QY 301 VQAAALSVSENPENMEGPERDQVLPDQBEQEAAGEGNQKLRGEDDYNNDENEASE 360
Db 302 VQAAALSVSENPENMEGPERDQVLPDQBEQEAAGEGNQKLRGEDDYNNDENEASE 361
QY 361 TDKQAAAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 400
Db 362 TDKQAAAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 401

RESULT 2
GP73 MOUSE
ID GP73 MOUSE STANDARD; PRT; 393 AA.
AC Q91XA2;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Golgi phosphoprotein 2 (Golgi membrane protein GP73).
GN Name=Golp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINE=FBV/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Unknown. Cellular response protein to viral infection
(By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Early Golgi.
CC Cycles via the cell surface and endosomes upon luminal pH
disruption (By similarity).
CC -!- INDUCTION: Up-regulated in response to viral infection (By
similarity).
CC -!- PTM: Glycosylated (By similarity).
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC -----
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CC -----
CC EMBL; BC011152; AAH1152.1; -
DR MGD; MGI:1917329; Golp2.

KW Coiled coil; Glycoprotein; Golgi stack; Signal-anchor; Transmembrane.
FT DOMAIN 1 12
FT TRANSMEM 13 35
FT Signal-anchor for type II membrane
FT protein (Potential).
FT lumenal (Potential).
FT DOMAIN 36 393
FT DOMAIN 40 183
FT CARBOHYD 109 109
FT CARBOHYD 144 144
FT CARBOHYD 227 227
FT N-linked (GlcNAc...) (Potential).
FT N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 393 AA; 44310 MW; B19897C9D6D3618F CRC64;

Query Match 59.0%; Score 1196.5; DB 1; Length 393;
Best Local Similarity 65.5%; Pred. No. 4.2e-49;
Matches 262; Conservative 51; Mismatches 68; Indels 19; Gaps 10;

QY 1 MGLNGRRSMKSPPLVLAALVACIVLGFNFWIASSRSVLDQTRIMELEGRVRRRAAERG 60
Db 2 MGLNGRRSMKSPPLVLAALVACIVLGFNFWIASSRSVLDQTRIMELEGRVRRRAAERG 61
QY 61 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITGGERLIRVLQ 120
Db 62 AVELKKNFQGELEKQREQLDKIQSSHNFOLESVKNLYQDEKAVLVNNITGGERLIRVLQ 121
QY 121 DQKTLQRYNCRLOQDVLFQKQNTLNKRSYDLSQINQWKEVKEQCEERIEVTKG 180
Db 122 DQKALQRSYSLQODIFQKQNTLSKFSYDLNQCSIQWTEVKEQCEERIEVIRKR 181
QY 181 NEAVASRLSENNDRQQQLAUSEPQRLQAAGLPHTEVPQKGNVLGNSKSTQTPAPSE 240
Db 182 NEAVASRLSENNDRQQQLAUSEPQRLQAAGLPHTEVPQKGNVLGNSKSTQTPAPSE 237
QY 241 VVLDKQVKEKETNEIQVNEEPQDRLPQBPQREQVVEDRVPVGRGFGGAGELGQTPQ 300
Db 238 -SLGLKPQVQNEETNEIQVNEEPQDRLPQBPQREQVVEDRVPVGRGFGGAGELGQTPQ 286
QY 301 VQAAALSVSENPENMEGPERDQVLPDQBEQEAAGEGNQKLRGEDDYNNDENEASE 360
Db 287 LPAGI-LARPEDSQYPEREQVLRD-RQEQRAAEGGGQK-NPGDEYDMENEASE 342
QY 361 TDKQAAAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 400
Db 343 REKQAAAGNDRNIDVFNVEDQKRTDINLLDQREKNHTL 382

RESULT 3
Q7ZUC8
ID Q7ZUC8 PRELIMINARY; PRT; 411 AA.
AC Q7ZUC8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein zgc:56525.
GN ORFNames=zgc:56525;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Unknown. Cellular response protein to viral infection
(By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Early Golgi.
CC Cycles via the cell surface and endosomes upon luminal pH
disruption (By similarity).
CC -!- INDUCTION: Up-regulated in response to viral infection (By
similarity).
CC -!- PTM: Glycosylated (By similarity).
CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC -----
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CC -----
CC EMBL; BC011152; AAH1152.1; -
DR MGD; MGI:1917329; Golp2.


```
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RC Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049324; AAH49324.1; -
DR ZFIN; ZDB-GENE-040426-1060; zgc:56525.
KW Hypothetical protein.
SQ SEQUENCE 411 AA; 45462 MW; 0521526362E3D29B CRC64;

Query Match 20.8%; Score 423; DB 2; Length 411;
Best Local Similarity 26.8%; Pred. No. 1.5e-12;
Matches 118; Conservative 96; Mismatches 124; Indels 102; Gaps 15;

QY 1 MG-LGNGRRSMKSPPLVLAALVACIIVLGFNYVIASSRVDLQTRIMELEGRVRAAER 59
DB 2 MGALNGRRGGRSPSLMAALISCIILAFNYVWSNRVELQSKILEDHIRLLSADR 61

QY 60 GAVELKNEFOGELEKREQLDKIOSSHNFOLESVKNLYQDEKAVLVNNTTGERLIRVL 119
DB 62 EREKSKLKAEDEMHROEQLEMEKTHRQOENAINSWRQENLQNLNLSAKAVQNM 121

QY 120 QDLKTLQRYGRLOQDVLPQKQNTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKK 179
DB 122 KNRKMSLLEDVNMKQSELKSSMDTLTKKANSDKTCQNKIEATKEECVVKI 175

QY 180 GNEAVASRDLSNNDRQOLALSEPQRLQAAGLPHTEVPQKGNVLGNSKSTPA-- 236
DB 176 ---AAA-----KQELKTAEKVDP--QDADGPEQKVLKAKSDVLALNKNPAEP 221

QY 237 PSSEVVLDSKQVEKE-ETNEIQVNVNBPQRDLRQPEPGRQVVDREDPVGGFGAGEL 295
DB 222 PNGKLDVDSPLNDAQVETNELV--EKDAKDAV-----ILQDTPIAASKLTNKSSET 271

QY 296 GOTPOVQA-----ALSVQENPEMGPEDQLVDPGQEEQEAAGEGRN 340
DB 272 LKPAFAEVAEVEDIKPAPKDAEVLDEADILE-PKENEAGIGDANEEDDVGIGDANQ 330

QY 341 QO-----KLRG-----EDD---Y 350
DB 331 EDDDELKLGADLKEEDAAGKEDAIMYDNEGEIEKQLSQIKDENQAGQDLEDDVANY 390

QY 351 N-MDENEAESETDKQAALAG 369
DB 391 NGDDENQPESEDEKQAEALAG 410

RESULT 4
Q6POHO PRELIMINARY; PRT; 410 AA.
AC Q6POHO;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Zgc:56525 protein.
GN ORFNames=zgc:56525;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RC Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065624; AAH65624.1; -
DR ZFIN; ZDB-GENE-040426-1060; zgc:56525.
SQ SEQUENCE 410 AA; 45332 MW; DC6BCBC54515EE25 CRC64;

Query Match 20.7%; Score 419; DB 2; Length 410;
Best Local Similarity 26.2%; Pred. No. 2.4e-12;
Matches 115; Conservative 94; Mismatches 130; Indels 100; Gaps 14;

QY 1 MG-LGNGRRSMKSPPLVLAALVACIIVLGFNYVIASSRVDLQTRIMELEGRVRAAER 59
DB 1 MGALNGRRGGRSPSLMAALISCIILAFNYVWSNRVELQSKILEDHIRLLSADR 60

QY 60 GAVELKNEFOGELEKREQLDKIOSSHNFOLESVKNLYQDEKAVLVNNTTGERLIRVL 119
DB 61 EREKSKLKAEDEMHROEQLEMEKTHRQOENAINSWRQENLQNLNLSAKAVQNM 120

QY 120 QDLKTLQRYGRLOQDVLPQKQNTNLERKFSYDLSQINQMKEVKEQCEERIEEVTKK 179
DB 121 KNRKMSLLEDVNMKQSELKSSMDTLTKKANSDKTCQNKIEATKEECVVKI 174

QY 180 GNEAVASRDLSNNDRQOLALSEPQRLQAAGLPHTEVPQKGNVLGNSKSTPA-- 236
DB 175 ---AAA-----KQELKTAEKVDP--QDADGPEQKVLKAKSDVLALNKNPAEP 220

QY 237 PSSEVVLDSKQVEKE-ETNEIQVNVNBPQRDLRQPEPGRQVVDREDPVGGFGAGEL 295
DB 221 PNGKLDVDSPLNDAQVETNELV--EKDAKDAV-----ILQDTPIAASKLTNKSSET 270

QY 296 GOTPOVQAALSVSOPENPEMG-----PERDQLVDPGQEEQEAAGEGRN 341
DB 271 LKPAFAEVAEVEDIKPAPKDAEVLDEADILE-PKENEAGIGDANEEDDVGIGDANQ 330

QY 342 Q-----KLRG-----EDD---YN 351
DB 331 EDDDELKLGADLKEEDAAGKEDAIMYDNEGEIEKQLSQIKDENQAGQDLEDDVANY 390

QY 352 -MDENEAESETDKQAALAG 369
DB 391 GDDENQPESEDEKQAEALAG 409

RESULT 5
Q641D4 PRELIMINARY; PRT; 355 AA.
AC Q641D4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
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QY 283 PVGG-----RGFGGAGELGOTPVQAALSVSQENPEMGPEDOLV----- 323
Db 289 FTGQPLSPMPDPSHININGPGTSKQNPSSPLQRLIPGSLNDSEPRIQTDTLLKQATKDR 348
QY 324 IPDQGE-----EFQEAAGEGRNQOKLGRGDDYNDME-NEASETDKQAALAGND 371
Db 349 VSDPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYEAADKAELAYNE 401

RESULT 7
Q6RZW6
ID Q6RZW6 PRELIMINARY; PRT; 402 AA.
AC Q6RZW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE VGF2573 isoform 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Shat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064446; AAB64446.1; -.
SQ SEQUENCE 435 AA; 49408 MW; C62F71B6B2FA7598 CRC64;

Query Match 17.0%; Score 345.5; DB 2; Length 435;
Best Local Similarity 26.0%; Pred. No. 7.5e-09;
Matches 115; Conservative 78; Mismatches 175; Indels 75; Gaps 12;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNFWIASRSVDLQTRIMELEGRRVRAAERG 60
Db 2 VGFANRRAGRLPSFVLVLLVIVLAFNFWYSSIRHVLQEEVAELQGVQVTEVARG 61

QY 61 AVELKKNFEQGELEKQREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVDTHTKKQIDQKEADYGRLSRLQAKEGLGKRCEDDKVKYLNNTSYQMA 121

QY 115 LIRVLQDLKTLQRYNGRLQODVLQFQKNQTNLERKFSYDLQSNQINOMKEVKEOCEERIE 174
Db 122 DIHHLKEQLAEFLQOEFLQEDQLQDYRKNTYLVKRLYESFQCCQQLKELRAQHEENIK 181

QY 175 EVTKKGNFQGELEKQREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNTTGER 114
Db 182 KLAQFLQEQKETHKIQSDGKE-----LGRNDHGAPKNI PNPENDANKN 227

QY 235 PAPSEVVLDSKRQVEKEETNIQVNEEPQDRRLP-----QSPGREQVVEDR 282
Db 228 EDPSSNHLPHGKEQLKRVGDAGMPGVEENDLAKVDELPAALKKPPVLAQSQESHQTIHSL 287

QY 283 PVG---GRGFGGAGELGOTPVQAALSVSQENPE-----MEGP---ERDQLVIPDQGE-- 329
Db 288 PTGQPLSPMAPGSHLNQENP-----STSKQNPSPNLOHIIPGNLDRPRIQTDTLLKQAT 343

QY 330 -----EEQEAAGEGRNQOKLGRGDDYNDME-NEASETDKQAALAGND 371
Db 344 TRDANDPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYEAADKAELAYNE 400

QY 372 RNIDVFNVEDQKRDITINLLDQRE 394
Db 401 BEDGDGGEVDVQDD-----ERE 418
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QY 283 PVGG-----RGFGGAGELGOTPVQAALSVSQENPEMGPEDOLV----- 323
Db 289 FTGQPLSPMPDPSHININGPGTSKQNPSSPLQRLIPGSLNDSEPRIQTDTLLKQATKDR 348
QY 324 IPDQGE-----EFQEAAGEGRNQOKLGRGDDYNDME-NEASETDKQAALAGND 371
Db 349 VSDPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYEAADKAELAYNE 401

RESULT 7
Q6RZW6
ID Q6RZW6 PRELIMINARY; PRT; 402 AA.
AC Q6RZW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE VGF2573 isoform 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Shat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY484583; AAR26704.1; -.
SQ SEQUENCE 402 AA; 45913 MW; 906EB9162B6A7F9A CRC64;

Query Match 17.2%; Score 348; DB 2; Length 402;
Best Local Similarity 26.5%; Pred. No. 5.2e-09;
Matches 116; Conservative 76; Mismatches 148; Indels 98; Gaps 15;

QY 1 MGLNGRRSMKSPPLVLAALVACIIVLGFNFWIASRSVDLQTRIMELEGRRVRAAERG 60
Db 2 VGFANRRAGRLPSFVLVLLVIVLAFNFWYSSIRHVLQEEVAELQGVQVTEVARG 61

QY 61 AVELKKNFEQGELEKQREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVDTHTKKQIDQKEADYGRLSRLQAKEGLGKRCEDDKVKYLNNTSYQMA 121

QY 115 LIRVLQDLKTLQRYNGRLQODVLQFQKNQTNLERKFSYDLQSNQINOMKEVKEOCEERIE 174
Db 122 DIHHLKEQLAEFLQOEFLQEDQLQDYRKNTYLVKRLYESFQCCQQLKELRAQHEENIK 181

QY 175 EVTKKGNFQGELEKQREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNTTGER 114
Db 182 KLAQFLQEQKETHKIQSDGKE-----KIQSDNGKELGRNDHGA 212

QY 235 PAPSEVVLDSKRQVEKEETNIQVNEEPQDRRLPQEPGRQVVEDRPGVGRGFGGAGE 294
Db 213 P-----KNIPNPENDANK-----NEDPSSNHLPH---GKEQL---KRVGDAGMPGVEE 255

QY 295 ---LGOTPVQQAAL-----SVSQENPE-----MEGP---ERDQLVIPDQGE----- 329
Db 256 NDIAKVDLQAPGSHLNQENPSTSKQNPSPNLOHIIPGNLDRPRIQTDTLLKQATRRA 315

QY 330 -----EEQEAAGEGRNQOKLGRGDDYNDME-NEASETDKQAALAGNDRTIDV 376
Db 316 NDFPHKLKQSRFFDENESVPDPQHGSKLA---DYNGDDGNVGEYEAADKAELAYNEEDGD 372

QY 377 FNVEDQKRDITINLLDQRE 394
Db 373 GGEEDVQDD-----ERE 385
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RESULT 8
Q6P2L7
ID Q6P2L7 PRELIMINARY; PRT; 435 AA.
AC Q6P2L7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE	VFGG2573 isoform 2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J;
RA	Zhou G., Liu X., Li H.;
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AY484585; AAR26705.1; -- D7D9308F3A2063FC CRC64;
SQ	SEQUENCE 319 AA; 36067 MW; D7D9308F3A2063FC CRC64;

Query Match	15.4%;	Score 312;	DB 2;	Length 319;
Best Local Similarity	26.9%;	Pred. No. 2e-07;		
Matches	97;	Conservative	64;	Mismatches 137; Indels 62; Gaps 12

Qy	1	MGLNGRRSMKSPPLVLAALVACIIIVLGFNTWIASSRVSVDLQTRIMELEGRRVRAAAERG	60
Db	2	VGFGANRRAGRLFSFVLVLLVIVLAFNYSISRRLVQLQEEVAELQGVQVQTEVARG	61
Qy	61	AVELKKNEFQGELEKQREQLDKIQ-----SSHNFOLESVNLQYDEKAVLVNNTTGTGR	114
Db	62	RLEKRNDDLLLVTHTKKQIDQKEADYGRUSSRLQAKELGKRCEDDKVKLQNNISQYMA	121
Qy	115	LIRVLQDLKTLQRYNGRLQODVLQFOKNQTNLTKRKFSDYDLSCQINOMKEVKEQCEERIE	174
Db	122	DIHHLKQLAELRQEFRLQEDLDQDYRKNTYLVKRLYESFQCGQQLKELRAQHEENIK	181
Qy	175	EVTYKKGNEAVASRDLSNNDRQQLQALSRPQLQAAGLPHTEVPQKGKGNVLGNSKQT	234
Db	182	K-----LADQPLQKQETH-----KIQSNDGKELGRNDHGA	212
Qy	235	PAPSSSVLDSKQVKEETNEIOVNVNEQDRDLPOEPGEVVEDRPGVGRGFGGAGE	294
Db	213	P-----KNIPNVENDANK-----NEDPSSNNLPH--GKEQL---KRVGDAGMPGVEE	255
Qy	295	--LQGTPOQAALSVSQ-ENP--EMEGPERD-QLVIP-----DGOBEEQEAAGEGRNQKL	344
Db	256	NDLAKVDLDPAGSHLNQENPFSKQNPSPLOHIIIPGNGSGTQNSNRHVYKAGHQGQSL	315

RESULT 11				
ID	Q8C422	PRELIMINARY;	PRT;	176 AA.
AC	Q8C422;			
DT	01-MAR-2003 (TReMBLrel. 23, Created)			
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)			
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)			
DE	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched			
DE	library, clone:A630071M09 product:hypothetical protein, full insert			
DE	sequence. (Fragment).			
GN	Name=D130060C09Rik;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;			
RA	Carninci P., Hayaishizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			


```

Qy 276 EQVVEDRVPVGGGFGGAGE-----LGQTPVQQAALSVSQENPEMGPGRDQVLPDQGE 329
Db 250 EDSJGN-DVKGQDTGALPSQSKSLKQPSLQ-PLSFTHEHYKPLPKKTKVQIP---E 304
Qy 330 BEQEAAGEGRNQKLRGDDDDNMDENAESETDKQAALAGNDRNDIVFN 378
Db 305 VEENALQLEPHLPKQMPDRSKTMSFNLKQKDDHDDQADAGEYKHDLN 353

RESULT 13
Q96EM1 ID Q96EM1 PRELIMINARY; PRT; 177 AA.
AC Q96EM1.
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE H63 protein.
DB 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012124; AAH12124.1; -.
SQ SEQUENCE 177 AA; 20934 MW; DF8452919A90949A CRC64;

Query Match 11.6%; Score 235; DB 2; Length 177;
Best Local Similarity 33.1%; Pred. No. 0.00045;
Matches 57; Conservative 37; Mismatches 70; Indels 8; Gaps 2;

Qy 1 MGLNGRRSMKSPPLVLAALVACILVLGFNFWIASSRSVDLQTRIMELEGVRRAAERG 60
Db 2 VGFGANRRAGRLPSLVLLVLLVILVAFNFWISRSSRVLLEQEEVAELQGGVQRTVARG 61
Qy 61 AVELKNGFEQLEKQRELDKIQ-----SSHNFOLESVNKLYODEKAVLVNNTTGER 114
Db 62 RLEKNSDLLLVTHKKQIDQKEADYGRLLSRRLQAREGLKRCDDKVLKNNISYQMA 121
Qy 115 LIRVLQDLKTLQRYGRLOQDLVLFQKQNTNLERKFSYDLS--QCINQMK 164
Db 122 DIHHLKEQLAEFLRQEDQLQDYRKNTYLVKRLYESKRPKRFNQME 173

RESULT 14
Q25142 ID Q25142 PRELIMINARY; PRT; 1927 AA.
AC Q25142.
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DB 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
OS Embryonic muscle myosin heavy chain.
CN Name=MHCEmb;
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Araki I., Satoh N.;
RT "Cis-regulatory elements conserved in the proximal promoter region of
RT an ascidian embryonic muscle myosin heavy chain gene.";
RL Roux's Arch. Dev. Biol. 0:0-0(1995).
DR EMBL; D45163; BAA08111.1; -.
DR PIR; A59236; A59236.
DR HSPF; P08799; IMND.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003774; F:motor activity; IEA.
DR InterPro; IPR000048; IQ region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR004009; Myosin_tail.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; Myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR SMART; SM00242; MYSC; 1.
SQ SEQUENCE 1927 AA; 222461 MW; 2F6F18A2B71BC34E CRC64;

Query Match 9.9%; Score 200.5; DB 2; Length 1927;
Best Local Similarity 23.1%; Pred. No. 0.29;
Matches 96; Conservative 57; Mismatches 151; Indels 111; Gaps 13;

Qy 40 DLQTRIMELEGVRRAAARGAVELKKNFQGELE----- 74
Db 1110 ELQARIELELEEAARAARAKVEKQADLSRELEELSERLEEAGGATAAQIENKREA 1169
Qy 75 ---KORQLDKIQSHNFQLESVNKLYODEKAVLVNNTTGERLIRVLQDLKTLQRYNG 131
Db 1170 EFSKLRELEESNLAHEATVSTLRKCHADSAEMSEQIDNLRQVKQLEKESEMKMEVD 1229
Qy 132 RLQODV-----LQFQKQNTNLERKFSYDLSQCINQMKVEKQCEERIEVTKKGN 184
Db 1230 DLAAANVESITKAKLVYKMAKNLEEQFSKTKCDNFCKEYNEL-----NAA 1276
Qy 185 ASRDLSENNDORQQLQALSEPPRLQAGLPHTVPGQKGNVLGNSKTSQTPAPSEVLD 244
Db 1277 KAFASENGELSRL-----EREHLMA-----QLTRTKNSSSQQIEE 1314
Qy 245 SKRQVEKETNEIQVNVNEEPQDRLPQSGREQVVEDRPGVGGFGGAGELGQTPVQAAA 304
Db 1315 LKRVVE-EETKAKAALAHVQASRDNDLLREQVEEQA-----KAEQRA 1360
Qy 305 LSVS-----QENPEMGPGRDQVLPDQGEQEA-----AGEGRNOOK 343
Db 1361 LSKANAESAQVQWRNKYETAIQRTTELEBAKKAATRLQEAEEQVEAQKASLDKTKNR 1420
Qy 344 LRGE-DDYNDENEAESQKQAALAGNDRNDID-VFNVEDOKRTINL-LDQREK 395
Db 1421 LQGELEDITID---LERSNSAAALDKQRNFDKVLAEKQKEBEIQVELSQAOK 1472

RESULT 15
Q75UE0 ID Q75UE0 PRELIMINARY; PRT; 1491 AA.
AC Q75UE0.
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

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Search completed: June 7, 2005, 14:07:33
Job time : 180 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:01:01 ; Search time 41 Seconds
(without alignments)
938.700 Million cell updates/sec

Title: US-10-759-803-2
Perfect score: 2029
Sequence: 1 MGLNGRRSMKSPPLVLAAL.....DQKRDITNLLDQREKRNHTL 400
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200.5	9.9	1927	2 A59236	embryonic muscle m
2	185	9.1	1974	2 T30010	hypothetical prote
3	178.5	8.8	1963	1 MKXW	myosin heavy chain
4	176	8.7	1200	2 S77524	chromosome segrega
5	176	8.7	3498	2 T22330	hypothetical prote
6	174	8.6	1738	2 T14867	interaptin - slime
7	172.5	8.5	1175	2 C35815	myosin heavy chain
8	172.5	8.5	1201	2 A35815	myosin heavy chain
9	172	8.5	1175	2 D35815	myosin heavy chain
10	172	8.5	1201	2 B35815	myosin heavy chain
11	171.5	8.5	1164	2 T24806	hypothetical prote
12	171.5	8.5	1938	1 A40987	myosin heavy chain
13	170.5	8.4	1940	2 A59287	myosin heavy chain
14	170	8.4	2385	2 A32491	myosin heavy chain
15	170	8.4	2411	2 B32491	myosin heavy chain
16	169.5	8.4	1269	2 F84730	probable myosin he
17	168.5	8.3	1938	2 A59293	skeletal myosin he
18	168	8.3	1922	2 T00637	hypothetical prote
19	167.5	8.3	1956	2 T16416	hypothetical prote
20	167.5	8.3	1957	2 A45627	myosin heavy chain
21	167	8.2	849	2 S00030	neurofilament trip
22	167	8.2	1961	1 A61231	myosin heavy chain
23	167	8.2	3187	2 JC5837	364K Golgi complex
24	166.5	8.2	1940	1 A24922	myosin heavy chain
25	166.5	8.2	1999	1 S21801	myosin heavy chain
26	166	8.2	895	2 T45738	hypothetical prote
27	166	8.2	944	2 S26710	spindle pole body
28	166	8.2	1938	1 JX0178	myosin heavy chain
29	165.5	8.2	1940	1 S04090	myosin heavy chain

30 165 8.1 876 2 A23767 myosin heavy chain
31 165 8.1 1898 1 A45973 trichohyalin - hum
32 165 8.1 1992 2 A47297 myosin heavy chain
33 164.5 8.1 1959 1 A33977 myosin heavy chain
34 164 8.1 1138 2 T24635 hypothetical prote
35 163.5 8.1 1957 2 A59294 skeletal myosin -
36 163.5 8.1 1957 2 T38077 hypothetical coile
37 163 8.0 1940 2 A29320 myosin heavy chain
38 162.5 8.0 798 2 T50479 neurofilament medi
39 161 7.9 1133 2 T22976 hypothetical prote
40 160.5 7.9 428 1 T36930 involucrin - white
41 160.5 7.9 916 2 A27884 neurofilament trip
42 160.5 7.9 2057 2 S61477 myosin II heavy ch
43 160 7.9 447 2 T46146 hypothetical prote
44 160 7.9 936 2 S39083 myosin heavy chain
45 160 7.9 980 2 E71606 hypothetical prote

ALIGNMENTS

RESULT 1

A59236
embryonic muscle myosin heavy chain - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59236
R:Araki, I.
submitted to GenBank, February 1999
A:Reference number: A59236
A:Accession: A59236
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1927 <ARA>
A:Cross-references: UNIPROT:Q25142; GB:D45163; NID:gl1197167; PIDN:BAA08111.1; PID:gl11971
A:Experimental source: clone lib lambda gtl1; dev stage tailbud embryo
C:Genetics:
A:Gene: MHCemb
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:89-766/Domain: myosin motor domain homology <MHO>

Query Match 9.9%; Score 200.5; DB 2; Length 1927;
Best Local Similarity 23.1%; Pred. No. 0.0082;
Matches 96; Conservative 57; Mismatches 151; Indels 111; Gaps 13;
Qy 40 DLQTRIMELEGRVRRRAERGAELKKNFQGELE----- 74
Db 1110 ELQARIEELEEAERAAKAEKQADLSRELEELSERLEAGGATAAIELNKRREA 1169
Qy 75 ---KQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNITTTGERLIRVLQDLQKLTQRYNG 131
Db 1170 EFSKLRLEESNLAHEATVSTLRKKHADSSAENSEQIDNLRVKQKLEKSEKMEVD 1229
Qy 132 RLQODV-----LQFOKQNTNLERKFSYDLSCQINQMKVEKCEERIEEVTKKGNRAV 184
Db 1230 DLAAVNESITKALNVEKMAKNLEEQFSSEKTKCDNFCKEYNEL-----NAA 1276
Qy 185 ASRDLSENNDORQQLALSEPQLQAAGLPHTEVPQKGNVLGNSKTSQTPAPSESVLD 244
Db 1277 KAPASENGSLROL-----EREHLMA-----QUTRTKNSSQQQLTEE 1314
Qy 245 SKRQVEKEETNEIOVNVNEEPQRLQEPQREQVVEDRPGVGRGFGGAGELGQTPQVQAA 304
Db 1315 LKRVVE-EETKAKAALAHSAQASRDNDLLREQVEESEA-----KAEQRA 1360
Qy 305 LSVS-----QENDEMGPERDQVLIPDQEEBEQA-----AGGRNOOK 343
Db 1361 LSKNAEVAQWRNKYETDAIQRTTEELEAKKCLATRLQEAEEQVEAEQAKCASIDKTKR 1420
Qy 344 LRGE-DDYNDNEAESETDKQALAGNDRNID-VFNVEDQKRTINL-LDQREK 395
Db 1421 LQGELEDLTID---LERSNSAAAALDKQRNFNDKVLAEKQKEEIQVELEQAOK 1472

RESULT 2

T30010
hypothetical protein F58G4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T30010
R:Du, Z.; Leimac, D.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid F58G4.
A:Reference number: Z20720
A:Accession: T30010
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1974 <DUZ>
A:Cross-references: UNIPROT:Q21000; EMBL:U50309; PIDN:AAB37057.1; GSPDB:GN000023; CESP:F58G4
A:Experimental source: strain Bristol N2; clone F58G4
C:Genetics:
A:Gene: CESP:F58G4.1
A:Map position: 5
A:Introns: 18/3; 111/3; 164/1; 229/1; 378/1; 440/2; 525/3; 1177/2; 1633/3; 1863/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:84-776/Domain: myosin motor domain homology <MMO>

Query Match 9.1%; Score 185; DB 2; Length 1974;
Best Local Similarity 22.3%; Pred. No. 0.054;
Matches 90; Conservative 75; Mismatches 144; Indels 94; Gaps 15;

QY 40 DIOTRIMELEGRVRRRAAARGAVELKKNEFOGELEKQREOLDKIQSSHNFOLE----- 92
Db 1120 ELLARIQLEELDAERNSRKAERKARNQMELGELGRLDEAGGATQAQIQLNKREA 1179

QY 93 SVNKLYQDEKAVLVNNTTGERL-----TRVLODQLKTLQRYNVRLOQDVLPQKNQT 145
Db 1180 ELAKLODLEADAAINSETSMALRKXNDVAELSDQDITQKMRGKLEKNDKQREVD 1239

QY 146 NLERKFSYDLSCINQMEKVEKQCEERIEVTKGNEAV-----ASRDLSENNDQR 196
Db 1240 ELQGSADVAKQRQN-CERMAKQLEAQTDMTLKSDQEARLQIQLTGWKKNVHNQDLN 1298

QY 197 QOQLALSBPQRLQAGLPHTEVPQKGNVLGNSKSTPAPSSEVVLDSKQKVEKETNE 256
Db 1299 RQLE---DAEAQLCA-----LNRIKQOQHSQLEEL---KRTLD-QETRE 1335

QY 257 IQVNEEPQRDLPLQEPGREQVVEDRPV-----GGRGFGGAGE 294
Db 1336 RQSLHSQVSNYQLECEQFRESLEERQDQKTDVQRLSKANSEIQOMRAKFEPEGVSRAEE 1395

QY 295 LGQTPQVQAALSVSQENPEMEGPERDQLVIPDQEEQEAAGEGRNQKLRGE-DDYNMD 353
Db 1396 LEETR-----KLTHKVQEMQ-----EQL-----ENANQIGTLEKKNQRLAHLDEDAQVD 1441

QY 354 ENEAES-ETDKQAALAGNDRNID-----VFNVEDQKRDY 386
Db 1442 ADTRANSIASLEKKQKGFQKVLDEWRKCEALVAEVEQSQRET 1484

RESULT 3

MKW
myosin heavy chain B [similarity] - Caenorhabditis elegans
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Caenorhabditis elegans
C:Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
A:Accession: T20770; T26229; A93958; A93287; A21074; A02992
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19322
A:Accession: T20770
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1963 <WIL>
A:Cross-references: UNIPROT:Q02244; EMBL:281499; PIDN:CAB04089.1; GSPDB:GN000019; CESP:F11C3
A:Experimental source: clone F11C3

A:Accession: T21629
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1963 <W12>

A:Cross-references: EMBL:283107; PIDN:CAB05505.1; GSPDB:GN000019; CESP:F11C3.3

A:Experimental source: Clone F32A7

R:Karn, J.; Brenner, S.; Barnett, L.

Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983

A:Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy chain

A:Reference number: A93958; MUID:83273600; PMID:6576334

A:Accession: A93958

A:Molecule type: DNA

A:Residues: 1-61, 'EMSVIQ', 65-376, 'V', 378-1963 <KAR>

A:Cross-references: GB:J01050; NID:g156399; PIDN:AAA28124.1; PID:g156400

R:McLachlan, A.D.; Karn, J.

Nature 299, 226-231, 1982

A:Title: Periodic charge distributions in the myosin rod amino acid sequence match cross

A:Reference number: A93287; MUID:82272395; PMID:7202124

A:Accession: A93287

A:Molecule type: DNA

A:Residues: 847-1333, 'R', 1335-1876, 'L', 1878-1963 <MCL>

R:Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H.

Cell 33, 575-583, 1983

A:Title: The genes sup-7 X and sup-5 III of Caenorhabditis elegans suppress amber nonsense

A:Reference number: A21074; MUID:83232892; PMID:6571695

A:Accession: A21074

A:Molecule type: DNA

A:Residues: 1873-1963 <W13>

A:Cross-references: GB:V01494; GB:J01049; NID:g6783; PIDN:CAA24738.1; PID:g6784

C:Genetics:

A:Gene: unc-54; CESP:F11C3.3

A:Map position: 1

A:Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle con

F:84-775/Domain: myosin motor domain homology <MMOT>

F:174-181/Region: nucleotide-binding motif A (P-loop)

F:662-684/Region: actin binding #status predicted

F:766-780/Region: actin binding #status predicted

F:848-1963/Domain: coiled coil #status predicted <COI>

F:848-1162/Region: S2

F:1163-1963/Region: light meromyosin

F:125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted

F:180/Binding site: ATP (Lys) #status predicted

F:702,712/Active site: Cys #status predicted

Query Match 8.8%; Score 178.5; DB 1; Length 1963;

Best Local Similarity 21.8%; Pred. No. 0.12;

Matches 90; Conservative 77; Mismatches 177; Indels 69; Gaps 13;

QY 40 DIOTRIMELEGRVRRRAAARGAVELKKNEFOGELEKQREOLDKIQSSHNFOLESVNKLYQ 99
Db 1119 DGQRISLEEELEENRQSRKADRAKSDLQRELEELGKLDQGGATAAQVE-VNKKRE 1177

QY 100 DEKAVLVNNTTGER-----LIRVLQDQLKTLQRYNVRLOQDVLPQKNQ 144
Db 1178 AELAKLRDLLEANNHENHNLGLRKKHTDAVELTDQLDQLNKAKAVKDKQAQRDA 1237

QY 145 TNLERKFSYDLSCINQMEKVEKQCEERIEVTKGNEAVASRDLSENNDQRLQALSE 204
Db 1238 EDLAAQLDQETSGKLNKLAK-QPELQTLQSKADE-----QSRQLQDFTS 1284

QY 205 PQPRLQAG---LPHTEVPQKGNVLGNSKSTPAPSSEVVLDSKQKVEKETNEIQVN 261
Db 1285 LKGRHLSENGDLVFRQLEDAESQVNLTRLKSQLTSLQLEEARRTADEEARERQITVAAQKN 1344

QY 262 EEPQRDLPLQEPGREQVVEDRPV-----GGRGFGGAGELGQTP----- 299
Db 1345 YQHEARQL-QESLEEEIEGKNEILLQLSKANADIQQWAKRFEGLLXKADELDAKRQA 1403

QY 300 ----QVQAAL-SVQENPEMEGPERDQLVIPDQEEQEAAGEGRNQKLRGDDVNM 352
Db 1404 QKINELQALDAANSKNASLE-KTKSRVLVGDLDDAQVDVERANGVASALEKKQKGFDKII 1462


```
Qy 72 ELEK-----QREOLDKIQSSHNFOLESVKN-----LYODEK--AVLVNNTTGRLL 115
Db 1197 DKDSQFTQLQDDQKQQLQSIQODLN-QLKQENQEKESKDEKLSIQIFEN-QREKQ 1254
Qy 116 IRVLQDQLKTTLRNRYGRLL-----QDVLQFQKQNTNLERKFSYDLSQCINQMKVEKQCEE 171
Db 1255 LSEKDEKLSIQNLNLDNENQEKVKQFSEKDEKLQ-----SIQDNLNQLKQENQEK 1309
Qy 172 RIEEVTKKGNNAVASRDLSE--NDORQOLQALSEPQRL-----QAAGLPHTEVP 220
Db 1310 QLSEKDEKLSQ-----IQDNLNLDNDQIKKNEKLKEKEBQLLQDQFNDDQSQQLKQLEK 1367
Qy 221 -QSGNVNLGNSKST-----PAPSSBVLDSKROVEKETNEIQVNVNEPQDRRLPOE 272
Db 1368 LSEKENQLQKQENQENQNLNQQOOSNEIIOQLKDLKQKQOQOQENNEKEIERLLQ 1427
Qy 273 PGREQVDRPVGGRFGAGELGTPQVQAALSVSQENPEMB-----GPERDQLVIPDQ 328
Db 1428 --IEQLKQQ-----EIDQSELNSKEIKIQTQQBFDQLSHNRSKDQLHLQQLQ 1474
Qy 329 EE-----BOEAAGEGRNQOKLGE--DDYNWDENEAE 358
Db 1475 QELDQLKQSFDDQHQPKVVIDERYNLQLEQSTLSNNQLDQLKEKLPLELDSNEKQ 1534
Qy 359 SETDKQAALAGN-----DRNIDVFNVEDQKRDNTINLLDQRE 394
Db 1535 KTIDLLSNISNLQISLQNDKDLISERNNSIKTLESRITQQLSLLDEKD 1583

RESULT 7
CJ35815
myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: C35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: A35815
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1175 <COL>
A:CROSS-references: UNIPROT:Q8IP00; UNIPROT:Q8IN29; EMBL:X53155; NID:g8219; PIDN:CAA3730
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:
A:Gene: FlyBase:Mhc
A:CROSS-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 8.5%; Score 172.5; DB 2; Length 1175;
Best Local Similarity 19.7%; Pred. No. 0.13;
Matches 83; Conservative 88; Mismatches 144; Indels 107; Gaps 14;

Qy 41 LQTRIMELEGRVRRRAAERGAVELKKNFQG-----ELEKQREOLDKIQSSHNQ 90
Db 265 LEQTLDELEDSLEREKVKRGDVEKSKRVKVEGDLKLTQEAVALDERNKKELEQTIQRKDKE 324
Qy 91 LESVNLKYDEKAVLVNNTTGERLIRVLQDQLKTLQRYNGRLQDVLQFQKN-----143
Db 325 LSSITAKLEDEQVVLKHK-----ORQIKELQARIEELEEEVEAEARQAKAEQORADLARE 380
Qy 144 -----QTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKGNNAVAS 186
Db 381 LEEELGERLEEAGGATSAQIELNKKREAEKSLRRDLEANIQHESTLANLRKKHNDAVA- 439
Qy 187 RDLSENNDORQOLQALSEPQRLQAGLPHTEVPQKGG--NVLGNSKSKQTPAPSEVILD 244
Db 440 -EMAEQVDQLNKLKAKAEHNRQ-----TCHNELNTRTACDQLGRDKA-----481
Qy 245 SKRQVEKE---ETNEIQVNVNEPQDRRLPOEPGRQV--VEDRPVGGRGFGAGELGQTQ 300
Db 482 AQEIKAKQLQHTLNEVQSKLDDETRNLNDFDASKKKKLSIENSDLLRLQLEAEESQVSLSK 541
Qy 301 VQAALVSQENPEMGPGRDQLVPDQBEQEQAAGEGRNQOKLGEDDDYND-----E 354
Db 542 IKISUTTOLEDTKRLADESR-----ERATLLGKFRNL-----EHDLDNLREQVE 586
Qy 355 NEAESETDKQAALAGNDRNIDVF-----NVEDQKR-----DTINLLD 391
Db 587 EEAEGKADLQRLSKANAQAQVWRKSYESDGVARSEELEAEAKRKLQARLAEAEETIESLN 646
Qy 392 QR 393
Db 647 QK 648
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Db 482 AQEIKAKQLQHTLNEVQSKLDDETRNLNDFDASKKKKLSIENSDLLRLQLEAEESQVSLSK 541
Qy 301 VQAALVSQENPEMGPGRDQLVPDQBEQEQAAGEGRNQOKLGEDDDYND-----E 354
Db 542 IKISUTTOLEDTKRLADESR-----ERATLLGKFRNL-----EHDLDNLREQVE 586
Qy 355 NEAESETDKQAALAGNDRNIDVF-----NVEDQKR-----DTINLLD 391
Db 587 EEAEGKADLQRLSKANAQAQVWRKSYESDGVARSEELEAEAKRKLQARLAEAEETIESLN 646
Qy 392 QR 393
Db 647 QK 648

RESULT 8
CJ35815
myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 12-Oct-1990 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: A35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A:Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: A35815
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1201 <COL>
A:CROSS-references: UNIPROT:O18392; EMBL:X53155; NID:g8219; PIDN:CAA37310.1; PID:g254693
A:Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:
A:Gene: FlyBase:Mhc
A:CROSS-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 8.5%; Score 172.5; DB 2; Length 1201;
Best Local Similarity 19.7%; Pred. No. 0.13;
Matches 83; Conservative 88; Mismatches 144; Indels 107; Gaps 14;

Qy 41 LQTRIMELEGRVRRRAAERGAVELKKNFQG-----ELEKQREOLDKIQSSHNQ 90
Db 265 LEQTLDELEDSLEREKVKRGDVEKSKRVKVEGDLKLTQEAVALDERNKKELEQTIQRKDKE 324
Qy 91 LESVNLKYDEKAVLVNNTTGERLIRVLQDQLKTLQRYNGRLQDVLQFQKN-----143
Db 325 LSSITAKLEDEQVVLKHK-----ORQIKELQARIEELEEEVEAEARQAKAEQORADLARE 380
Qy 144 -----QTNLERKFSYDLSQCINQMKVEKQCEERIEEVTKKGNNAVAS 186
Db 381 LEEELGERLEEAGGATSAQIELNKKREAEKSLRRDLEANIQHESTLANLRKKHNDAVA- 439
Qy 187 RDLSENNDORQOLQALSEPQRLQAGLPHTEVPQKGG--NVLGNSKSKQTPAPSEVILD 244
Db 440 -EMAEQVDQLNKLKAKAEHNRQ-----TCHNELNTRTACDQLGRDKA-----481
Qy 245 SKRQVEKE---ETNEIQVNVNEPQDRRLPOEPGRQV--VEDRPVGGRGFGAGELGQTQ 300
Db 482 AQEIKAKQLQHTLNEVQSKLDDETRNLNDFDASKKKKLSIENSDLLRLQLEAEESQVSLSK 541
Qy 301 VQAALVSQENPEMGPGRDQLVPDQBEQEQAAGEGRNQOKLGEDDDYND-----E 354
Db 542 IKISUTTOLEDTKRLADESR-----ERATLLGKFRNL-----EHDLDNLREQVE 586
Qy 355 NEAESETDKQAALAGNDRNIDVF-----NVEDQKR-----DTINLLD 391
Db 587 EEAEGKADLQRLSKANAQAQVWRKSYESDGVARSEELEAEAKRKLQARLAEAEETIESLN 646
Qy 392 QR 393
Db 647 QK 648
```

RESULT 9
D35815
myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: D35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A>Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: D35815
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1175 <COL>
A:Cross-references: UNIPROT:Q9TY21; EMBL:X53155
A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:
A:Gene: FlyBase:Mhc
A:Cross-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 8.5%; Score 172; DB 2; Length 1175;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 84; Conservative 73; Mismatches 155; Indels 96; Gaps 11;

Qy 41 LQTRIMELEGVRVRAAARGAVELKKNFQG-----ELEKQRLDKIQSSHNQ 90
Db LEQTLDELEDSLERKKVGDVEKSKVGGDLKLTQAVADLERKKELEQTQKDK 324
Qy 91 LESVNVLYODEKAVLVNNTTGERLIRVLQDLKTLQRYGRLOQDVLQFQKN-----143
Db LSSITAKLEDEQVVLKH-----QRQIKELQARIEELEVEAEARQAKAKQADLARE 380
Qy 144 -----QTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKGNEAVAS 186
Db LEEGERLEEAGGATSAQIELNKKREAEKSLRDLEEANTQHESTLANLRKCHNDAVA- 439
Qy 187 RDLSENNDQROLOALSEPQRLQ-----AAGLPH-----TEVP 220
Db -EMAEQVDOLNKLKAKAEKNEYVQGLNDRAGVDHITNEKAAQEKIAQLOHTLNEV- 497
Qy 221 QGKGNVLGNSKSTPPAPSEVVLDK---RQVEKEETN-----EIQVNVNEEPPQDRRLP 270
Db QSKLDETNRITLNDPASKKLSIENSLLRQLEAEASQVLSKIKISLTITQLEDTKRLA 557
Qy 271 QEPGREQVVEDRPGVGRFGGAGELGQTPQVQAALSVSQENPEMGPEDQIVPDQGE 330
Db DEESRER-----ATLLGKFRNLHDLNLRREQVEEAEKADL-----QRQ 598
Qy 331 EQEAAAGEGRNOQKLRGDDYNNDENEAESETDKQAALAGNDRNIDVFN 378
Db LSKANAEOVWRSKYVESGVARSELEAKKQLQARLAEABETIESLN 646

RESULT 10
B35815
myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: B35815
R:Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A>Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A:Reference number: A35815; MUID:90346288; PMID:2116987
A:Accession: B35815
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1201 <COL>
A:Cross-references: UNIPROT:O18392; EMBL:X53155; NID:98219; PIDN:CAA37311.1; PID:9254693
A>Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C:Genetics:

A:Gene: FlyBase:Mhc
A:Cross-references: FlyBase:FBgn0002741
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP

Query Match 8.5%; Score 172; DB 2; Length 1201;
Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 84; Conservative 73; Mismatches 155; Indels 96; Gaps 11;

Qy 41 LQTRIMELEGVRVRAAARGAVELKKNFQG-----ELEKQRLDKIQSSHNQ 90
Db LEQTLDELEDSLERKKVGDVEKSKVGGDLKLTQAVADLERKKELEQTQKDK 324
Qy 91 LESVNVLYODEKAVLVNNTTGERLIRVLQDLKTLQRYGRLOQDVLQFQKN-----143
Db LSSITAKLEDEQVVLKH-----QRQIKELQARIEELEVEAEARQAKAKQADLARE 380
Qy 144 -----QTNLERKFSYDLSCINQMKVEKQCEERIEEVTKKGNEAVAS 186
Db LEEGERLEEAGGATSAQIELNKKREAEKSLRDLEEANTQHESTLANLRKCHNDAVA- 439
Qy 187 RDLSENNDQROLOALSEPQRLQ-----AAGLPH-----TEVP 220
Db -EMAEQVDOLNKLKAKAEKNEYVQGLNDRAGVDHITNEKAAQEKIAQLOHTLNEV- 497
Qy 221 QGKGNVLGNSKSTPPAPSEVVLDK---RQVEKEETN-----EIQVNVNEEPPQDRRLP 270
Db QSKLDETNRITLNDPASKKLSIENSLLRQLEAEASQVLSKIKISLTITQLEDTKRLA 557
Qy 271 QEPGREQVVEDRPGVGRFGGAGELGQTPQVQAALSVSQENPEMGPEDQIVPDQGE 330
Db DEESRER-----ATLLGKFRNLHDLNLRREQVEEAEKADL-----QRQ 598
Qy 331 EQEAAAGEGRNOQKLRGDDYNNDENEAESETDKQAALAGNDRNIDVFN 378
Db LSKANAEOVWRSKYVESGVARSELEAKKQLQARLAEABETIESLN 646

RESULT 11
T24806
hypothetical protein T10G3.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24806
R:Burton, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19937
A:Accession: T24806
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1164 <WIL>
A:Cross-references: UNIPROT:P92021; EMBL:Z81118; PIDN:CA03330.1; GSPDB:GN00023; CESP:T1
A:Experimental source: clone T10G3
C:Genetics:
A:Gene: CESP:T10G3.5
A:Map position: 5
A:Introns: 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2

Query Match 8.5%; Score 171.5; DB 2; Length 1164;
Best Local Similarity 19.6%; Pred. No. 0.15;
Matches 87; Conservative 80; Mismatches 154; Indels 123; Gaps 16;

Qy 3 LGNRRRSMKPPVLAAALVACIIIVGFNYTASSRSVDLQTRIMELEGVRVRAAARGAV 62
Db IGEGETVKQ-----LQISYDAQSELKQERNVVOLEARI-----EENVF 341
Qy 63 ELKQNE-----FQGELEKQK---EOLDKIOSSHNQFLESVNVKLYODEKAVLVNNTTGER 114
Db ELSENKQNVKRLDKVQESQDALQMLSNINGSNEEQMISLNSKFERNTAERKRTAEAVPEE 401
Qy 115 LIRVLQDLKTLQRYGRLOQDVLQ-----FQKQNTNLERKFSYDLSCINQMKVEKQCE 170
Db KTVQGERLKTLEMANLDLTNELASMGSLDKERSLLEEK-NKEISRDSSINDLKEKLA 460

R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.

Mol. Cell. Biol. 9, 2957-2974, 1989

A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene
A:Reference number: A32491; MUID:89384556; PMID:2506434

A:Accession: B32491

A>Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-2385 <GEO>

A:Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194

A>Note: the authors translated the codon TGC for residue 329 as Ser

C:Genetics:

A:Gene: FlyBase:Mhc

A:Cross-references: FlyBase:FBgn0002741

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; nucleotide binding; P-loop

F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>

F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 8.4%; Score 170; DB 2; Length 2385;
Best Local Similarity 20.9%; Pred. No. 0.41;
Matches 86; Conservative 77; Mismatches 148; Indels 100; Gaps 14;

Qy 41 LQTRIMELEGRVRAAARGAVELKNEFGQ-----ELEKQREOLDKIQSSHNQ 90

Db 1449 LEQTLDELEDSLEREKVKRGDVEKSKRVGDLKLTQEA VADLERNKKELEQTQKDK 1508

Qy 91 LESVNLKYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGLRQDVLQFQKN----- 143

Db 1509 LSSITAKLEDEQVVVLKH-----QRQIKELQARIIELEEEVEAEQRAKAEQKQADLARE 1564

Qy 144 -----QTNLERKFSYDLSCINQMKEVKQCEERIEEVTYKKGNEAVAS 186

Db 1565 LEELGERLEEAGGATSAQIELNKKREAELSKLRDLEEA NTQHESTLANLRKKHNDAVA- 1623

Qy 187 RDLSENNDROQLQALSEPQPRLOAAGLPHTVEPQGVKGNVLGNSKSTPPASSEVVLDSK 246

Db 1624 -EMAEQVDQLNKLKAKAE-----HNR-----QTCNHLNQTRTACDQLGRD-K 1664

Qy 247 RQVEKEE-----TNEIQ-----VNEEPQDRRLPOEPGRQVVEDRPVGGRGFGGAGELGQ 297

Db 1665 AEKEKNEYGQLNDLRAGVDHITNEKAAQEKI-----AKQLQH 1702

Qy 298 T-PQVQAALSVSQENPEMGPEDQVLPDG-----QEEQEAAGGRNQKLRGEDDYNM 352

Db 1703 TLNEVQSKLDENRTNLFDFDASKKLSIENSDDLRLQLEEAESQVSQLSKISLTQLED 1762

Qy 353 DENEAESETDKQAALAGNDRNI--DVFN-----VEDQKRDITNLLDQREKN 397

Db 1763 TKRLADEESRERATLLGKFRNLEHDLNLRQVEEAEGKADLQRLQSKAN 1813

RESULT 15

B32491

myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

A:Accession: B32491

R:George, E.L.; Ober, M.B.; Emerson Jr., C.P.

Mol. Cell. Biol. 9, 2957-2974, 1989

A:Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene
A:Reference number: A32491; MUID:89384556; PMID:2506434

A:Accession: B32491

A>Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-2411 <GEO>

A:Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194

A>Note: the authors translated the codon TGC for residue 329 as Ser

C:Genetics:

A:Gene: FlyBase:Mhc

A:Cross-references: FlyBase:FBgn0002741

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; nucleotide binding; P-loop

F:137-1032/Domain: myosin motor domain homology #status atypical <MMO>

F:227-234/Region: nucleotide-binding motif A (P-loop)

Query Match 8.4%; Score 170; DB 2; Length 2411;

Best Local Similarity 20.9%; Pred. No. 0.42;

Matches 86; Conservative 77; Mismatches 148; Indels 100; Gaps 14;

Qy 41 LQTRIMELEGRVRAAARGAVELKNEFGQ-----ELEKQREOLDKIQSSHNQ 90

Db 1449 LEQTLDELEDSLEREKVKRGDVEKSKRVGDLKLTQEA VADLERNKKELEQTQKDK 1508

Qy 91 LESVNLKYQDEKAVLVNNTTGERLIRVLQDLKTLQRYNGLRQDVLQFQKN----- 143

Db 1509 LSSITAKLEDEQVVVLKH-----QRQIKELQARIIELEEEVEAEQRAKAEQKQADLARE 1564

Qy 144 -----QTNLERKFSYDLSCINQMKEVKQCEERIEEVTYKKGNEAVAS 186

Db 1565 LEELGERLEEAGGATSAQIELNKKREAELSKLRDLEEA NTQHESTLANLRKKHNDAVA- 1623

Qy 187 RDLSENNDROQLQALSEPQPRLOAAGLPHTVEPQGVKGNVLGNSKSTPPASSEVVLDSK 246

Db 1624 -EMAEQVDQLNKLKAKAE-----HNR-----QTCNHLNQTRTACDQLGRD-K 1664

Qy 247 RQVEKEE-----TNEIQ-----VNEEPQDRRLPOEPGRQVVEDRPVGGRGFGGAGELGQ 297

Db 1665 AEKEKNEYGQLNDLRAGVDHITNEKAAQEKI-----AKQLQH 1702

Qy 298 T-PQVQAALSVSQENPEMGPEDQVLPDG-----QEEQEAAGGRNQKLRGEDDYNM 352

Db 1703 TLNEVQSKLDENRTNLFDFDASKKLSIENSDDLRLQLEEAESQVSQLSKISLTQLED 1762

Qy 353 DENEAESETDKQAALAGNDRNI--DVFN-----VEDQKRDITNLLDQREKN 397

Db 1763 TKRLADEESRERATLLGKFRNLEHDLNLRQVEEAEGKADLQRLQSKAN 1813

Search completed: June 7, 2005, 14:11:01

Job time : 44 secs

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